

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 138939

TO: Terra Gibbs

Location: rem/2d10/2c18

**Art Unit: 1635** 

Tuesday, December 07, 2004

Case Serial Number: 09/491063

From: Peggy Ruppel

Location: Biotech-Chem Library

**REMSEN 1B65** 

Phone: 571-272-2557

Peggy.Ruppel@uspto.gov

#### Search Notes

The results of your sequence search request are attached. Please contact me if you have any questions or comments.

Thank you for using STIC services.



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#### STIC-Biotech/ChemLib

ノ From:

Gibbs, Terra

Sent:

Tuesday, November 30, 2004 10:11 AM

To:
Subject:

STIC-Biotech/ChemLib
Sequence search request...

Could you please do a regular search of SEQ ID NO:1 of USSN 09/491063 in all commercial and pending databases? Could you please do a regular search of SEQ ID NO:2 of USSN 09/491063 in all commercial and pending databases?

Terra Cotta Gibbs, Ph.D. Art Unit 1635 Remsen Building 2D10 Mailbox 2C18 571-272-0758

STAFF USE ONLY

Online Time:

Searcher: \_\_\_\_\_Searcher Phone: 2-Date Searcher Picked up: \_\_\_\_\_Date Completed: \_\_\_\_\_\_Searcher Prep/Rev. Time: \_\_\_\_

\*\*\*\*\*\*\*\*

Type of Search

NA Sequence: #\_\_\_\_\_\_

AA Sequence : #\_\_\_\_\_\_

Structure: #\_\_\_\_\_\_

Bibliographic: \_\_\_\_\_\_

Litigation: \_\_\_\_\_\_

Patent Family: \_\_\_\_\_\_

Other:

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Vendors and cost where applicable STN:\_\_\_\_\_

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WWW/Internet:\_\_\_\_\_
Other(Specify):\_\_\_\_\_

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
9: gb_pr:*
9: gb_ro:*
10: gb_ro:*
11: gb_sts:*
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Gapop 10.0 , Gapext 1.0
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1083
1 atgcccccaccaaa
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10739.095 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

### ALIGNMENTS

rep_origin	CDS	gene		source	FEATURES	PUBMED	MEDI.TUE	TOTRNAT.	TITLE	AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION		DEFINITION	Locus	RESULT 1
/gene="ALL" //gene="ALL" //gene="ALL" //gote="putative" //codon_start=1 //codon_start=1 //product="replicative protein" //product="replicative protein" //protein_id="AAC32414.1" //protein_id="AAC32414.1" //db_xref="GI:295321" //db_xref="GI:295321" //db_xref="GI:295321" //db_xref="GI:295321" //db_xref="GI:295321" //db_xref="GI:295321" //db_xref="GI:295321" //db_xref="GI:295421" //db_xref="GI:29	complement (join(15232601,17))	/note="A component" complement(join(15232601,17))	/organism="Tomato mottle virus-[Florida]" /mol_type="genomic DNA" /db_xref="taxon:223359"	1 1 1	Location/Qualifiers		3107858	I Gen Virol 73 (Pt 12) 3225-3229 (1992)	The nucleotide sequence of tomato mottle virus, a new geminivirus	I (Dases I to 2601) Abouzid,A.M., Polston,J.E. and Hiebert,E.	Viruses; ssDNA viruses; Geminiviridae; Begomovirus.	Tomato mottle virus-[Florida]	Tomato mottle virus-[Florida]	•	L14460.1 GI:295320	(AL2), and AL3 genes, complete cds.	virus-[Florida] complete A co	TMWALR 2601 bp ss-DNA circular VRL 07-MAR-2003	

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                                                         CCAGAGGAGGCCAGCCTGCTAATGATTCATATGCGAAAGCATTAAATGCAGGTTCGG
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SVASPQSLPELPSLDDVDDSFWINLFS"
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/gene="AL2"
complement (1222. .1611)
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complement (1077. .1475)
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complement (1077. .1475)
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yrkprwyrtlattdvaagcegpckvQsspqnbishigkwglisbvtrgwgithlygk
recyksvyilakimwbenikikikmthisvmymburpsptgtpwbibtwtpwmpdnbspt
atvkndlrdryQvmikfygkvtggQyasneQaivkrfwkvnnhvvynhQeagkyenht
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NNVVRAVRFATNRVYVNHVLENHSIKFKFY"
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/codon_start=1
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325. .1080
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Gilbertson,R.L., Hidayat,S.H., Paplomatas,E.J., Rojas,M.R.,
Hou,Y.M. and Maxwell,D.P.
Pseudorecombination between infectious cloned DNA components
tomato mottle and bean dwarf mosaic geminiviruses
J. Gen. Virol. 74 (Pt 1), 23-31 (1993)
                                                                                                                                                                                                                                                                            Gilbertson, R.L., Hidayat, S.H., Rojas, M.R. and Maxwell, Infectious DNA clones of a new geminivirus associated
                                                                                                                                                                                                                                                                                                                                                   Tomato mottle virus
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Tomato mottle virus replicative
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                                                                                                                                                                                                                                                                                                                    (Bites)
/organism="Tomato mottle virus"
/mol_type="genomic DNA"
/strain="FL-B1"
                                                                          Location/Qualifiers
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VRL 24-MAY-2001

1083

1762 847 1822

1882

1702

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CTCAGTGGACACCTAGACTTCAATGGTCGAGTCTTCTCGAATGATGTGCAGTATAACGTC
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/codon_start=1
/codon_start=1
/product="replicative protein"
/product="replicative protein"
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QNHNIRSNLERIFAKAPEPMVPPFQVSSFTNVPDEMQEWADNYFGTGAAARPERPVSI
IVEGDSRTGKTWWARALGPHNYLSGHLDFNGRVFSNDVQYNVIDDIAPHYLKLKHWKE
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IFITLTAPLYQDSTQASQETGNQKAQG"
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/function="replication"
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Matches 1061; Conserv
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Sequence 1 f
AR170763
AR170763.1
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Stout, J.T., Luu, H.T., Hanson, S.F., Maxwell, D.P., Ahlquist, P.G. Gilbertson, R.L.
                                                                                                                                                                                                                                                                                                                                                                 Transgenic plants expressing mutant Patent: US 6291743-A 1 18-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Unknown
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             CCAACCCCGGTCAGCACATTTCCATCCGAATATTCAGGGAGCTAAATCGAGCTCCGACGTC
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                                                                                                                  AAGAAATTCATCAAAATTTGCAGAGAGCTTCATGAAAATGGGGGAACCTCATCTCCATGTG
                                                                                                                                                 TGCTCTTTGTCTAAAGAAGAAGCACTTTCCCAATTACAAAACCTAAATACCCCAGTCAAT 163
                                                                                                                                                                                                               ATGCCCCCACCAAAAAATTTTAGAGTTCAGTCAAAGAACTATTTCCTAACTTATCCCCAG
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CCAACCCGGTCAGCACATTTCCATCCGAATATTCAGGGAGCTAAATCGAGCTCCGACGTC
                                                 CTTGTTCAGTTCGAAGGAAAGTACCAGTGCACGAATAACAGATTCTTCGACCTGGTCTCC
                                                                                                AAGAAATTCATCAAAATTTGCAGAGAGCTTCATGAAAATGGGGAACCTCATCTCCATGTG
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/mol_type="unassigned DNA"
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patent US 6291743.
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Sequence 5 :
AR170765
AR170765.1
1 (bases 1 to 1169)
Stout, J.T., Luu, H.T., Hanson, S.F., N
Gilbertson, R.L.
Transgenic plants expressing mutant
Patent: US 6391743-A 5 18-SEP-2001;
Location/Qualifiers
                                     Unclassified
                                            Unknown
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                                                                                                                                                                                                                                                                                                                     GCCCCCCTATCAAGAGAGCACACAGGCAAGCCAAGAAACGGGCAATCAGAAGGCGCAG
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patent US
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Best Local Similarity
Matches 1059; Conserv
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      CAAAATCATAACATCCGCTCTAACCTAGAACGAATATTCGCAAAGGCTCCGGAACCGTGG
                                                                                                                                                                                                             GGTTCGGTTCAATCTGCCTTAGCGGTTCTAAGGGAAGAACAACCAAAAGATTTTGTATTA
                                                                                                                                                                                                                                                                                                                                        AAGAAATTCATCAAAATTTGCAGAGAGATCTCATGAAAATGGGGAACCTCATCTCCATGTG
                                                                                                                                                                                                                                                                                                                                                                 ATGCCCCCACCAAAGAAATTTAGAGTTCAGTCAAAGAACTATTTCCTAACTTATCCCCAG
                                                       AAATCATACATCGACAAGGACGGAGATACAATCGAATGGGGAGATTTTCCAAATCGACGGC
                                                                                                                                                                                                                                                                                                               CTTGTTCAGTTCGAAGGAAAGTACCAGTGCACGAATAACAGATTCTTCGACCTGGTCTCC
                                                                                                          GAGGGTGATTCAAGAACAGGGCACACGATGTGGGCACGTGCGTTAGGCCCCACATAACTAT
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                                                                                                                                                                                                                                                                                        CCAACCCGGTCAGCACATTTCCATCCGAATATTCAGGGAGCTAAATCGAGCTCCGACGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                   96.5%;
nilarity 97.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="unknown"
/mol_type="unassigned
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1044.6;
Pred. No. 7.5e
0; Mismatches
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7.5e-292;
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283 300 343 360 403

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540 540 583 600 643 660 703

763

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DEFINITION
ACCESSION
VERSION
KEYWORDS
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JOURNAL
FEATURES
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AUTHORS
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AR170766
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Best Local Similarity
Matches 1058; Conserv
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Sequence 7
AR170766
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Stout, J.T., Luu, H.T., Hanson, S.F., Maxwell, D.P., Ahlquist, P.G.
Gilbertson, R.L.
Transgenic plants expressing mutant geminivirus AC1 or C1 genes
Patent: US 6291743 A 7 18-SEP-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown.
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                                                                                                                                                                                                                                                                                                                                                                    ATGCCCCCACCAAAGAAATTTAGAGTTCAGTCAAAGAACTATTTCCTAACTTATCCCCAG
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            CAAAATCATAACATCCGCTCTAACCTAGAACGAATATTCGCAAAGGCTCCGGAACCGTGG
                                                        AGATCTGCCAGAGGAGGCCAGCAGTCTGCTAATGATTCATATGCGAAAGCATTAAATGCA
                                                                                                                                     ANATCGTACATCGACAAGGACGGAGATACAATCGAATGGGGAGATTTCCAGATCGACGGC
                                                                                                                                                 AAATCATACATCGACAAGGACGGAGATACAATCGAATGGGGAGATTTCCAAATCGACGGC
                                                                                                                                                                                CCAACCCGGTCAGCACATTTCCATCCGAATATTCAGGGAGCTAAATCGAGCTCCGACGTC
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                                            AGTTCGGTTCAATCTGCCTTAGCAGTTCTAAGGGAAGAACAACCAAAAGATTTTGTATTA
                                                                                         AGATCTGCCAGAGGAGGCCAGCAGTCTGCTAATGATTCATATGCGAAAGCGTTAAATGCA
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/mol_type="unassigned
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Pred. No. 2.2e-291;
0; Mismatches 25;
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LOCUS
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SOURCE
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AUTHORS
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Best Local Similarity
Matches 1054; Conserv
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Sequence 17
AR170774
AR170774.1
                                                                                                                                                                                                                                                                   Unknown.
Unknown.
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                                                                                                                                                                               Transgenic plants expressing mutant Patent: US 6291743-A 17 18-SEP-2001; Location/Qualifiers
                                                                                                                                                                                                                  Unclassified.

1 (bases 1 to 2602)

1 (bases 1 to 2602)

Stout, J.T., Luu, H.T., Hanson, S.F., Maxwell, D.P., Ahlquist, P.G.
Gilbertson, R.L.
                                    GTTCCTCCATTTCAAGTCTCTTCATTTCACTAACGTTCCTGACGAGATGCAGGAATGGGCGGTTCCTCCATTTCAAGTCTCTTTCACTAACGTTCCTGACGAGATGCAGGAATGGGCGGTTCCTCCATTTCAAGTCTTCTTTCACTAACGTTCCTGACGAGATGCAGGAATGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGAAAATACAGGTCTCAAGAAACTGGACTATCAAGAATGCGATCTTCATCACCCTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGCAATCGTGCTTTGCAATCCTGGTGAGGGTGCCAGCTATAAAGAGTTCTTAGACAAA
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TATCTAAAGAAGAAGCACTTTCCCCAATTACAAAACCTAAATACCCCAGTCAACAAGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                     GGT 1083
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                                                                                     Conservative
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                                                                                                                                             /organism="unknown"
/mol_type="unassigned
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98.0%;
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                                                                                  Score 1040.8; DB 6;
Pred. No. 1e-290;
0; Mismatches 22;
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US 6291743
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RESULT 7
AR170764
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AR170764
Sequence 3 from p
AR170764
AR170764.1 GI:1
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                                                                                                                  ATACAGGTCTCAAGAACTGGACTATCAAGAATGCGATCTTCATCACCCTCACAGGCCCCCC 1027
                                                                                                                                                                                            ACATCGCACCGCATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTGGGGGGCCCAGAAAG
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                                                                                                                                                       TCGTGCTTTGCAATCCTGGTGAGGGTGCCAGCTATAAAGAGTTCTTAGACAAAGCAGAAA
                                                                                                                                                                 TCGTGCTTTGCAATCCTGGTGAGGGTGCCAGCTATAAAGAGTTCTTAGACAAAGCAGAAA
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                                                                             TCTATCAAGACAGCACACAGGCAAGCCAAGAAACGGCGCAATCAGAAGGCGCAGGGT
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  GI:17908723
                    patent
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Query Match 96.0%;
Best Local Similarity 97.5%;
Matches 1056; Conservative
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Stout, J.T., Luu, H.T., Hanson, S.F., M
Gilbertson, R.L.
Transgenic plants expressing mutant
Patent: US 6291743-A 3 18-SEP-2001;
Location/Qualifiers
                                                                                                              ATGCCCCCACCAAAGAAATTTAGAGTTCAGTCAAAGAACTATTTCCTAACTTATCCCCAG
ATTGATGACATCGCACCGCATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTGGGGGCC
                                                                                                                                                                                             GATAATTATTTCGGGACGGGTGACGCTGCGCCGCCGGATAGACCTGTAAGTATCATCGTC
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                                                                   CTCAGTGGACACCTAGACTTCAATGGTCGAGTCTTCTCGAATGATGTGCAGTATAACGTC
                                                                                                                                                                             GATAATTATTTCGGGACGGGTGCAGCTGCGCGGCCAGAGAGACCTGTAAGTATCATCGTC
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/mol_type="unassigned
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Pred. No. 1.9e-290;
0; Mismatches 27;
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Stout, J.T., Luu, H.T., Hanson, S.F., Maxwell, D.P.,
Gilbertson, R.L.
Transgenic plants expressing mutant geminivirus A
Patent: US 6291743-A 13 18-SEP-2001;
Location/Qualifiers
1. .1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown
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                                                                               ATGCCCCCACCAAAGAAATTTAGAGTTCAGTCAAAGAACTATTTCCTAACTTATCCCCAG
                                                                                                                                                                                                        AAGAAATTCATCAAAATTTGCAGAGAGACTTCATGAAAATGGGGGAACCTCATCTCCATGTG
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     A----GATCTGCCAGAGGAGGCCAGCAGTCTGCTAATGATTCATATGCGAAAGCATTAAA
                              ANATCGTACATCGACAAGGACGGAGATACAATCGAATGGGGAGATTTCCAGATCGACGGC
                                               AAATCATACATCGACAAGGACGGAGATACAATCGAATGGGGAGATTTCCAAATCGACGGC
                                                                                                                                                                                          AAGAAATTCATCAAAATTTGCAGAGAGCTTCATGAAAATGGGGAACCTCATCTCCATGTG
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/mol_type="unassigned
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AF049336 2605550
2 (bases 1 to 2642)
Abouzid, A.M., Polston, J.E. and Hiebert, E.
Direct Submission
Submitted (19-FEB-1998) Plant Pathology, University of Florida,
                                                                   Sida golden mosaic virus Sida golden mosaic virus Viruses, Begomovirus. Viruses, BesDNA, viruses, Geminiviridae, Begomovirus. 1 (bases 1 to 2642) Abouzid, A.M., Polston, J.E. and Hiebert, E. Molecular characterization of a geminivirus infectisantaremensis in Florida
                                                      Unpublished
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                                                                                                                                                                                                                                                                    /Codon_start=1
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                                                                                                                                                                /gene="AC4"
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                                                                                                                                                                                                                    complement (2228.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="AC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="transactivator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="AC2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAC05154.1"
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isolate="Florida"
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GCCCCCCTATCAAGAGAGACACACAGGCAAGCCAAGAAAACGGGCAATCAGAAGGCGCAG
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                                                                           GCAGAAAATACAGGTCTCAAGAACTGGACTATCAAGAATGCGATCTTCATCACCCCTCACA 1020
                                                                                                                                                 CCAGCAATCGTGCTTTGCAATCCTGGTGAGGGTGCCAGCTATAAAGAGTTCTTAGACAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATAATTATTTCGGGACGGGTGACGCTGCGCCGCCGGATAGACCTGTAAGTATCATCGTC 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAAATCATAACATCCGCTCTAACCTAGAACGAATATTCGCAAAGGCTCCGGAACCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATTCTGTTCAATCTGCCTTAGCGGTTTTAAGGGAAGAACAGCCAAAAGATTTTGTCTTG 2163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGATCTGCCAGAGGAGGCCAGCAGTCTGCTAATGATTCATATGCGAAAGCATTAAATGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTGTTCAGTTCGAAGGTAAGTACCAATGCACGAATAACAGATTCTTCGACCTGGTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGCCACCGCCAAAGAATTTAGAGTTCAGTCCAAAAACTATTTGGTCACTTATCCACAG
                                                        GAGGAAAATACAGGTCTCAGGAACTGGACTATCAAGAATGCGATCTTCATCACCCTCACA
                                                                                                                              CCAGCAATCGTGCTTTGCAATCCTGGTGAGGGTGCCAGCTATAAAGAGTTCCTAGACAAG
                                                                                                                                                                                                   CAAAAAGATTGGCAGTCAAATTGCAAATACGGCAAGCCAGTTCAAATTAAAGGTGGAATC
                                                                                                                                                                                                                                                                           ATTGATGACGTCGCACCGCAATATCTAAAGCTAAAGCACTGGAAAGAATTGCTGGGGGCC
                                                                                                                                                                                                                                                                                                         ATTGATGACATCGCACCGCATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTGGGGGCC
                                                                                                                                                                                                                                                                                                                                               GAAGGTGATTCAAGAACAGGGAAGACGATGTGGGCCACGTGCGTTAGGCCCACATAATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTCCTCCATTTCAACTCTCTCTTTCACTAACGTTCCCCGACGAGGATGCAAGAATGGGCG
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1622 GCCCCCCTCTATCAAGCAAGCACACAGGCAGGCCAAGAGGAGGGCCATACGGAGGCGGAG 1563

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Submitted (26-JUL-1989) Jeske H., Institut f Allgemeine Botanik,
Submitted (26-JUL-1989) Jeske H., Institut f Allgemeine Botanik,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (14-NOV-2003) Jeske H., Biologisches Institut, Pfaffenwaldring 57, D-70550 Stuttgart, GERMANY On Nov 21, 2003 this sequence version replaced gi:59349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        revised by [4]
4 (bases 1 to 2632)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (29-NOV-1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The nucleotide sequence of abutilon mosaic virus reveals prokaryotic as well as eukaryotic features Virology 178 (2), 461-468 (1990)
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1 (bases 1 to 2632)
Frischmuth, T., Zimmat, G. and Jeske, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abutilon mosaic virus Abutilon mosaic virus
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Abutilon mosaic virus subgenome
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                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:38490457
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YIDKDGDTAEWGEFQIDGRSARGGQQTANDSYAKALNAGDVQSALNIIKEEQPKDYVL
QNHNIRSNLERIFAKAPEPWVPRFPLSSFTAVPEEMQEWADDYFGSGSAARPDRPLSL
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/gene="ORF C1"
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LLGAQKDWQSNCKYGKPVQI KGGI PAI VLCNPGEGSSYKEYLDKEENTGLRNWTLKNA
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/specific host="Abutilon sellovian
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                                                                                                                                                                                                                                                                                                                                                                                           translation="MPPPKKFRVQAKNYFLTYPQCSLTKDEALSQLQNLETPVNKKFI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /segment="DNA A"
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                                                                                                                                                                                                                                                             ATCAMAATTTGCAGAGAGCTTCATGAAAATGGGGAACCTCATCTCCATGTGCTTGTTCAG
                             ATCGACAAGGACGGAGATACAATCGAATGGGGAGATTTCCAAATCGACGGCAGATCTGCC 369
                                                                                               TCAGCACATTTCCATCCGAATATTCAGGGAGCTAAATCGAGCTCCGACGTCAAATCATAC 309
                                                                                                                                                  TTCGAAGGCAAATACCAATGCACGAATAACAGATTCTTCGATCTGGTCTCCCCAACCAGG
                                                                                                                                                                       TTCGAAGGTAAGTACCAATGCACGAATAACAGATTCTTCGACCTGGTCTCCCCCAACCCGG
                                                                                                                                                                                                                        ATCAAGATCTGTAGAGAGCTTCACGAGAATGGGGAGCCTCATCTCCATGTGCTCATACAG
                                                                                                                                                                                                                                                                                                  ACTAAAGATGAGGCACTTTCCCAATTACAAAACCTAGAAAACCCCAGTGAACAAGAAGTTC
                                                                                                                                                                                                                                                                                                                                       TCTAAAGAAGAAGCACTTTCCCAATTACAAAACCTAAATACCCCAGTCAACAAGAAATTC
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                                                                          TCAGCACATTTCCATCCAAACATACAGGGAGCTAAATCCAGCTCCGACGTCAAGTCCTAC
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ATVKNDLRDRYQVLHKFYGKVTGGQYASNEQAIVKRFWKVNNHVVYNHQEAGKYENHT
ENALLLYMACTHASNPVYATLKIRIYFYDSLMN"
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1606~1607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="15.9 kDa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'product="14.4 kDa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="15.9 kDa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="ORF V1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 856.4; DB 14;
Pred. No. 3.7e-237;
0; Mismatches 136;
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KEYWORDS
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                                                                                JOURNAL
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                                            Direct Submission
Submitted (12-MAR-1996) Plant Pathology,
Heav Honolulu, HI 96822, USA
                                                                                                                                                                                                                                                                                                                                                                                                            AMU51137
Abutilon
                                                                                                                                                                                          1 (bases 1 to 2634)
Wu,Z.C.Hu.J.S.Polston.J.E., Ullman,D.E. and Hiebert,E.
Complete nucleotide sequence of a non-vector transmiss
                                                                                                                of abutilon mosaic geminivirus
Phytopathology 86 (6), 608-613 (1996)
2 (bases 1 to 2634)
Wu,Z.C.Hu,J.S.Polston.J.E., Ullman,D.
                                                                                                                                                                                                                                                                                                                                                                 complete cds.
U51137
                                                                                                                                                                                                                                                                                   Abutilon mosaic virus-HW
Abutilon mosaic virus-HW
                                                                                                                                                                                                                                                                Viruses; ssDNA viruses; Geminiviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCGCACCGCATTATCTAAAAGCTAAAAGCACTGGAAAAGAATTGCTGGGGGCCCCAGAAAGAT 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAATCTGCCTTAGCGGTTCTAAGGGAAGAACAACCAAAAAGTTTTTGTATTACAAAATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATCAAGAGAGCACACAGGCAAGCCAAGAAACGGGCAATCAGAAGGCGCAGGGT 1083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCGCACCGCACTATCTAAAGCTAAAGCACTGGAAAGAATTGCTGGGGGCCCAAAAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACCTGGACTTCAATGGTCGCGTCTATTCGAACGAAGTGGAGTATAACGTCATTGATGAC 1853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAAGGACAGGAAGACGATGTGGGCACGTTAGGCCCACATAACTATCTCAGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAAGAACAGGGAAGACGATGTGGGCGCGTGCGTTAGGCCCACATAACTATCTCAGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACATCCGCTCTAACCTAGAACGAATATTCGCAAAGGCTCCGGAAACGTTGGGTTCCTCCA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATCAAGAAGGCACACAGGCCAGGCCAAGAGGAGGCCCATTAGGCGGCGGAGGAT 1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAGGTCTCAAGAACTGGACTATCAAGAATGCGATCTTCATCACCCTCACAGCCCCCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGCTTTGCAATCCTGGTGAGGGTGCCAGCTATAAAGAGTTCTTAGACAAAGCAGAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGCAATCAAATTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATCCCAGCAATC 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACCTAGACTTCAATGGTCGAGTCTTCTCGAATGATGTGCAGTATAACGTCATTGATGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCGGGACGGGTGACGCTGCGCCGCCGGATAGACCTGTAAGTATCATCGTCGAGGGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACATCCGCTCCAATCTCGAAAGAATATTCGCAAAGGCTCCGGAACCATGGGTTCCGCGG 2093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCAGTCAAATTGCAAGTACGGCAAGCCGGTTCAAATTAAAGGAGGAATCCCAGCAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTCCCCTCTCCTCTTCACGGCCGTTCCCGAGGAGATGCAGGAGTGGGCGGATGATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTCAAGTCTCTTCTTTCACTAACGTTCCTGACGAGATGCAGGAATGGGCGGATAATTAT
                                    Way, Honolulu, HI 9682.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                            mosaic virus-HW AV1,
organism="Abutilon mosaic virus-HW"
                                                                                                                                                                                                                                                                                                                                                  GI:1657740
                                                                                                                                                                                                                                                                                                                                                                                                            2634 bp
1 AV1, AC3,
                                                                                                                      Ullman, D.E.
                                                                                                                                                                                                                                                                                                                                                                                                         AC2,
                                                                                                                                                                                                                                                              Begomovirus.
                                                                                                                                                                                                                                                                                                                                                                                                       circular VRL 07-MAR-2003 AC1, and AC4 genes,
                                                                                                                      and
                                                                              University of Hawaii,
                                                                                                                      Hiebert
                                                                                                                                                                                                       transmissible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1793
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Best Local Similarity
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                                                                              928;
                                        10
                     CCAAAGAAATTTAGAGTTCAGTCAAAGAACTATTTCCTAACTTATCCCCAGTGCTCTCTA
CCAGAGAAATTTAGAGTACAGGCCAAAAATTATTTCCTCACATATCCCCAGTACTCTCTT
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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/product="coat_protein.1"
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/FREDRIYLATADVPRGCYGYTGGQVASNEQSIVKRFWKVNNHVVYNHQEAGNYENHT
ENALLLYMACTHASNPVYATLKIRIYFYDSLMN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (1257.
/gene="AC2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mdsrtgelitvrqaengvytwgiknplyfrmykveeplytrtki
YHVQIRFNHNLRRALHLHKAYLNFQVWTTSMKASGSTYLARFTRLVNMYLDQLGVISI
NNVIRAVQFATDRSYVNYVLENHSIKFKFY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MPPPEKFRVQAKNYFLTYPQYSLAKEVALSQLQNLETPVNKKFI
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YIDKDGDTAREWGEFQIDGRSTRGKARAFHRPLSL
QNHAIRSNLERIFAKAPEPWVPPFPLSFTAVPEEMQEWADDYFGSGAAAFHRPLSL
IVEGDSRTGKTMWARALGPHNYLSGHLDFNGRVYSNEVLYNVIDDVAPQYLKLKHWKE
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/trānslation="MGSLISMCSYSSKANSNARIIDSSIWSPQPGQHISIQTYRELNR
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                                                                                                                                                                                                                                                                                                                                              SVASPQSLPELPSLDDIDESFWVNLFS" complement (2229. .2486)
                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="mrssspshppsikkahrqakrrairrrridlqcgcsiyfhidct
GHGFTHRGTHHCTSGGEWRVYLGDKKSPVFQDVQSRRTIIHQNENIPCTNTVQPQPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (1112. .1510)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (1112. .1510)
                                                                                                                                                                                                                                                                                                          complement (2229. .2486)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (1257. .1646)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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/db_xref="GI:1657742"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(1558. .2634,1.
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                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAB18172.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IFITLTSPLYQESTQAGQEEGNQTAED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="AC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="A component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /specific_host="Abutilon"
/db_xref="taxon:222059"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="Hawaii"
                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                   gene="AC4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            function="required for virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="AC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    function="involved in virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="AC3"
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db_xref="GI:1657744"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (26-OCT-1998) Plant Pathology, Davis, One Shields Ave., Davis, CA 95616, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              crumple geminivirus (in) ANNUAL MEETING OF PHYTOPATHOLOGY, VOL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jiang, H., Hou, Y.-M., Guzman, P. and Gilbertson, R.L. Complete nucleotide sequence of the infectious clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssDNA viruses; Geminiviridae; Begomovirus 1 (bases 1 to 2634)
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Chino del tomate virus-[IC]
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                                                                                                                                                                                                        /translation="mpsvkrpkvsaknyfltypqcslskgealsqlqtlktpvnkkyi
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yidkdgdtvemgefqlsgrarggqqsanstaklapsvqsamavlkeeqpkdpvl
hnhirsnlerifakaperwypfqlssptnydemqemaddyfgrgsakaperpisi
jugddsrtgktmmakalgphnylsghldfnpkyysneveynviddvaphylklkhmke
                                                                                                                                                                                                                                                                                                                                                                                     SVASPQSLPELPSLDDIDDSFWVDLFS" complement (1416. .2501)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tranblation="mpkrdlpwrsiagtskysrnanysprggsgprinkaaewynrpm
yrkpriyrtlatedwrrgcegockyosyeorhdishtgkymcisdytrongithrygk
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/db_xref="GI:4336697"
/translation="MRMGSLISTFSSNSKGSTSARITDSSIWSPQPGQHISIRTYREL
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                                                                                                            /codon_start=1
/product="AC4_protein"
                                                                                                                                                    complement (2087.
                                                                                                                                                                    LLGAQKDWQSNCKYGKPVQIKGGIPAIVLCNPGEGASYKDFLNKEENASLRNWTIKNA
IFITLTSALYQDSAQASQEKGHQEEAD"
                                                                                                                                                                                                                                                                                                     /product="AC1 protein"
/protein_id="AAD17898.1"
/db_xref="GI:4336694"
                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MRSSSPSHPPSIKTAHRQAKKRAIRRRRIDLRCGCSIYFHIGCT|
GHGFTHRGIHHCTSGGEWRYYLGDRKSPLFQDVQSGGSTVYENQGLPRSDTVQPQPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (1115. .1504)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mdsrtgefitvpqaengvyiweienplyfkmykvedlpytrtrv
yhvqirfnhnlrralhlhkaylnfqvwttsmiasgstylarfrhlvnmyldqlgvisi
nnviravrfatdrsyvsyvlenhsikfkly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="AC2 protein"
/protein_id="AAD17899.1"
/db_xref=[:4336695"
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/protein_id="AAD17900.1"
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/product="AV1 protein"
/protein_id="AAD17902.1"
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Direct Submission
Submitted (20-MAY-2003) Ramos P.L., P
Submitted (20-MAY-2003) Ramos P.L., P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cordero, M., Ramos, P.L., Hernandez, L., Echemendia, A.L., Peral, R., Gonzalez, G. Estevez, A. and Hernandez, K. Identification of Tomato mottle Taino potato fields
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AC1 gene; AV1 gene; coat protein;
Tomato mottle Taino virus
Tomato mottle Taino virus
Viruses; ssDNA viruses; Geminiviri
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kicrelhengephlyvlygegkytchnnffdlysptrsakfpniggaksssbykt
yinkdgdtlewgefqidgrsarggqqsandsykaklingnyqsamavlkeeqpkbfykt
yinknirsnlerifakapepwypfplssftnyddemoewadvyfgagsakrpnkemsi
viegdsrtgkymwaralgphnylsghldpntrysndvqynviddiaphylklkhwke
Llgaqrdwqsnckygkpvqikggipaivlcnpgegasykdflskdentslrdwtikna
/trānslation="mpkrdrtwrslagtskysrnanysprtgsgpignkasewynrpm
yrkpkiyrmmrtpdyprgcegpckyqsyeqrhdishygkymcyseytrgngithrygk
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/db_xref="GI:31044059"
                                                                                                                           /gene="AV1"
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/product="replicase"
/protein_id="CAD91703.1"
/db_xref="GI:31044058"
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/isolate="Boyeros"
/specific_host="Solanum
/db_xref="taxon:223358"
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AAGAACTGGACTATCAAGAATGCGATCTTCATCACCCTCACAGCCCCCCCTCTATCAAGAG
                                      AATCCTGGTGAGGGTGCCAGCTATAAAGACTTCCTCAGCAAAGACGAGAACACATCTCTC
                                                            AATCCTGGTGAGGGTGCCAGCTATAAAGAGTTCTTAGACAAAGCAGAAAATACAGGTCTC
                                                                                                               AACTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATCCCAGCAATCGTGCTTTGC
                                                                                                                                             AATTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATCCCCAGCAATCGTGCTTTGC
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Pred. No. 4.8e-228;
0; Mismatches 150;
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Tomato mottle Taino virus component
AF012300
AF012300.1 GI:2317786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-JUL-1997) Ingenieria Genetica, Apdo Postal 629, Irapuato, Gto 36500, Mexico
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taino tomato mottle virus, a new bipartite geminivirus from Cuba
Plant Dis. (1997) In press
2 (bases 1 to 2597)
2 (bases 1, Oramas, P., Guevara-Gonzalez, R. and Rivera-Bustamante, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; seDNA viruses; Geminiviridae; Begomovirus
1 (bases 1 to 2597)
Ramos,P.L., Guerra,O., Peral,P., Oramas,P., Guevar,
Rivera-Bustamante,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tomato mottle Taino virus
Tomato mottle Taino virus
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                                                                                        /translation="MRCSSPSQPPSIKIAHRQGKKRAIRRRRVDLQCGCSIYFHLNCA
GHGFTHRGTHHCTSGGEWRVYLGNTKSPLFQDVQSRGLAVHQNQGIPRTNTIQPQPBE
SVASPQSLPELPSLDDIDDSFWINIFS"
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/db_xref="G1:2317788"
/db_xref="G1:2317788"
/translation="mbsrtgelitahQAENGVYIWEIQNPLYFKMYRVEDLLFTRTRV
/translation="mbsrtgelitahQAENGVYIWEIQNPLYFKMYRVEDLLFTRTRV
YHAQIRFNHNLRRALHLHKAYLNFQVWTTSTTASGSTYLARFRELVNMYLDQIGVISI
NNVIRAVRFAINRAYVNYVLENHSIKFKFY"
                                                                            1387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mpkrdrtwrsiagtskvsrnanysprtgsgpignkasewvnrpm
yrkpkiyrmmrtpdvprgcegpckvqsyeqrhdishvgkvmcvsdvtrgngithrvgk
rfcvksvyiigkimmdeniklknhtnsvmfmlvrdrrpygtpmdfgqvfmmydnebst
                complement(1387.
/note="AL1, Rep"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATVKNDLRDRYQVMHRFHTKVTGGQYASNEQALVRRFWKVNNHVVYNHQEAAKYENHT
ENALLLYMACTHASNPVYATLKIRIYFYDSILN"
                                                      /gene="rep"
                                                                                                                                                   /codon_start=1
/product="transactivator
/protein_id="AAD09667.1"
/db_xref="GI:2317789"
                                                                                                                                                                                                                                complement (1086.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="AL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="coat protein"
/protein_id="AAD09665.1"
/db_xref="GI:2317787"
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/note="isolated from C
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                                                                                                                                                                                                                                                  'gene="TrAP"
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/db_xref="taxon:223358"
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Guevara, R.G.

CINVESTAV Irapuato,

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07-MAR-2003

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Query Match
Best Local Sim
Matches 913;
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                                                                                                                                                                                                                                                                                                                                                                       TCGTCTTTCACTAACGTTCCCGATGAGATGCAAGAGTGGGCGGATGTTTATTTTGGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTAGCGGTTCTAAGGGAAGAACAACCAAAAGATTTTGTATTACAAAATCATAACATCCGC
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AATTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATCCCAGCAATCGTGCTTTGC
                                                                               CATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTGGGGGCCCAGAAAGATTGGCAATCA
                                                                                                                                                                TTCAATGGTCGAGTCTTCTCGAATGATGTGCAGTATAACGTCATTGATGACATCGCACCG
                                                                                                                                                                                                       GGGAAGACGATGTGGGCCGTGCGTTAGGCCCACATAATTATCTGAGTGGACATTTGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAAATCTAGAAAGAATATTCGCCAAGGCTCCGGAACCATGGGTTCCTCCGTTTCCCCTC
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/translation="MPRKGSFSVKAKNYFLTYDQCSLSKEEALSQIQNLNTPVDKKFI
/translation="MPRKGSFSVKAKNYFLTYDQCSLSKEEALSQIQNLNTPVDKKFI
/translation="MPRKGSFSVKAKNYFLTYDQCSLSKEEALSQIQNLNTPVDKYFI
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HNHNIRSNLERIFAKAFAKAFNRFWSI
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LIGAQDEWQSNCKYGKEVQIKGGIPATYLCNPGEGASYKDFLSKDENTSLRDWTIKNA
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. No. 4.2e-227;
ismatches 152;
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Plant Dis. 72, 866-869 (1988)

2 (bases 1 to 2635)

2 (bases 1 to 2635)

Brown,J.K., Ostrow,K.M., Idris,A.M. and Stenger,D.C.

Chino del tomate virus: relationships to other begomoviruses

Chino del tomate virus relationships to ather begomoviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AP226664 Chino del tomate virus-[H8] variant H8 coat protein (AV1), replication enhancement protein (AC3), transcriptional activator protein (AC2), replication initiator protein (AC1), and AC4 genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phytopathology 90, 546-552 (2000) 3 (bases 1 to 2635) Stenger, D.C. and Brown, J.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssDNA viruses; Ger
1 (bases 1 to 2635)
Brown, J.K. and Nelson, M.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (20-JAN-2000) USDA-ARS,
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Chino del tomate virus-[H8]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmission, host range, and virus-vector relationships of chino del tomate virus, a whitefly-transmitted geminivirus from Sinaloa.
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                                                                    344 Keim Hall,
                 complement (971.
                                    /gene="AC3"
                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
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/db_xref="taxon:222454"
/chromosome="DNA A"
                                                                                                                                                                                                                                                                                                                               'gene="AV1"
                                                                                                                                                                                                                                                                                                                                                                     'note="variant H8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Chino del
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VE 68583, USA
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AAATCATACATCGACAAGGACGGAGATACAATCGAATGGGGAGATTTCCAAATCGACGGC
                                                                                   CCAACCCGGTCAGCACATTTCCATCCGAACATACAGGGAGCTAAATCCAGCTCCGACGTC
                                                                                                                                    CCAACCCGGTCAGCACATTTCCATCCGAATATTTCAGGGAGCTAAATCGAGCTCCGACGTC
                                                                                                                                                                                                                                        CTCATACAATTCGAAGGGAAGTACCAGTGCACGAATAACAGATTCTTCGATCTGGTCTCC
                                                                                                                                                                                                                                                                                                                   CTTGTTCAGTTCGAAGGTAAGTACCAATGCACGAATAACAGATTCTTCGACCTGGTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCTCTCTATCTAAAGAAGAAGCACTTTCCCCAATTACAAAACCTAAATACCCCAGTCAAC
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/COOOD BEAT = 1
/COOOD BEAT = 1
/COOOD BEAT = 1
/PROBLET = "TRANSCRIPTIONAL ACTIVATOR PROTEIN"
/PROTEIN_Id="ARF36704.1"
/PROTEIN_Id="ARF36704.1"
//DEAT = "GI:7109262"
//DEAT = "GI:7109262"
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/HTANBLATION="MRSSSPSHPSIKTH"
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/HTANBLATION="MRSSSPSHPSIKTH"
/HTANBLATION="MRSSSPSHPSIKTH"
/HTANBLATION="MRSSSPSHPSIKTH"
/HTANBLATIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (2088.
/gene="AC4"
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KICRELHENGEPHLHVLIQFEGKYQCTNNRFFDLVSPTRSAHFHDNIQAKSSDVKS
YIDKDGDTVEWGEFOLDGRSARGGQOSANDSYXKALNAGSVQAAMTULKEEQPKDFVLI
HNHNIRSNLERIFAKAPERWVPPFQLSSFTNVPDEMQEWADDYFRKSSAARPERPISI
I VEGDSRTGKTMWARALGPHNYLSGHLDFNPKYYSNEVEYNVIDDVAPHYLKLKHWKE
LLGAQKDWGSROKKYGKRVQIKGGIPATUKOPGEGASYKDFLNKEENASLRNWTIKNA
IFITLTSALYQDSAQASQEEGHQEEAD"
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NNVIRAVHFATDRSYVNYVLENHSIKFKLY"
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/db_xref="GI:7109261"
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84.7%;
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                                                                                                                                                                         GCAGAAAATACAGGTCTCAAGAACTGGACTATCAAGAATGCGATCTTCATCACCCTTCACA 1020
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                                                                   TCCGCCCTCTATCAAGACAGCGCACAGGCAAGCCAAGAAGAGGGCCCATCAGGAGGAGGCG
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                             atgcccccaccaaagaaatt....gcaatcagaaggcgcagggt 1083
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Aat93296 Bean gold
Aaa94702 pTrep23 n
Aat93291 Bean gold
Aaa94701 pTrepN nu
Aat93291 Bean gold
Aat93292 Bean gold
Aat93293 Bean gold
Aan60611 Vector se
Aaq84378 Tomato ye
Aaq12906 Sardinian
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50.2	80.2	158	162	183.8	185.2	238.2	243.8	246.6	251	259.4	259.4	259.4	304.4	418.4	419.6	421.2	448	474	476.2	479.4	479.4	479.4	492.8
4.6	7.4	14.6	15.0		17.1	22.0	22.5	22.8	23.2	24.0	24.0	24.0	28.1	38.6	38.7	38.9	41.4	43.8	44.0	44.3	44.3	44.3	45.5
795	270	434	297	479	780	550	550	1403	550	808	506	506	691	2744	1083	2723	2766	2739	1145	1145	1145	1145	1080
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AAZ49876	AA084370	AAQ84371	AAN70900	AAQ84372	AAT93319	AAQ84376	AAQ84377	AAT93318	AAQ84375	ABV76264	ABV76263	ABV76265	ABV76266	AAT93317	AAN70897	AAN70893	AAV29761	AAZ11646	AAT93289	AAT93311	AAT93288	AAT93287	AAT12904
Wheat	Aag84370 Gemini vi	Aaq84371 Gemini vi	Aan70900 ORF 7 fro	Aaq84372 Gemini vi	Aat93319 Tomato-in	Aaq84376 Tomato le	Aaq84377 Tomato le	Tomato	Aaq84375 Tomato le	Abv76264 Tomato ye	Abv76263 Tomato ye	Abv76265 Tomato ye	Abv76266 Tomato ye	Aat93317 Tomato le	Aan70897 ORF 4 fro	Aan70893 MYMV stra	Aav29761 Tobacco l	Aaz11646 Tomato le	Aat93289 Tomato ye	Aat93311 Tomato ye	Aat93288 Tomato ye	Aat93287 Tomato ye	Aat12904 Sardinian

### ALIGNMENTS

RESULT 1
AAT93294
ID
AAT93294 Tomato mottle virus AC1 open reading frame 17-OCT-2003 27-APR-1998 WO9739110-A1 Tomato mottle virus; isolate Florida Geminivirus; ToMoV; ACl gene; transdominant mutation; transgenic plant; disease resistance; ss; cyclic; circular. AAT93294; AAT93294 standard; DNA; 1160 BP. (revised) (first entry) 44. .1129 /\*tag= a Location/Qualifiers

15-APR-1997; 23-OCT-1997. 97WO-US006300

16-APR-1996; 96US-0015517P.

(SEMI-) SEMINIS VEGETABLE SEEDS INC. (WISC ) WISCONSIN ALUMNI RES FOUND.

Stout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;

WPI; 1997-526447/48. P-PSDB; AAW34332.

Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mottle virus, tomato yellow leaf curl virus or bean golden mosaic geminivirus.

Example 3.3; Page 57-58; 132pp; English.

This genomic DNA sequence includes the open reading frame of the wild-

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Query Match
Best Local Similarity
Matches 1061; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bipartite genome. The AC1 gene must be expressed for efficient replication of the two genomic components, DNA-A and DNA-B. It encodes a protein (see AAW34336) having a DNA binding site specific to the DNA-A common region, a DNA nicking activity, and an NTP binding activity. The invention involves production of transgenic plants containing DNA comprising AC1 or C1 wild-type or mutant sequences that negatively interfere in trans with geminiviral replication during infection. Such transgenic plants are resistant to viral infection. The AC1/C1 genes are especially from ToMoV, tomato yellow leaf curl virus or bean golden mosaic geminivirus (see AAT93282-93) and encode polypeptides (see AAW34324-35) that have mutations in the highly conserved DNA-nicking domain and/or the NTP-binding domain. (Updated on 17-OCT-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1160 BP; 360
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                                      CTCAGTGGACACCTAGACTTCAATGGTCGAGTCTTCTCGAATGATGTGCAGTATAACGTC
                                                                                   GATAATTATTTCGGGACGGGTGACGCTGCGCCCGCCGGATAGACCTGTAAGTATCATCGTC
                                                                                                                                                                                                                                                                                        GTTCCTCCATTTCAAGTCTCTTTCTTTCACTAACGTTCCTGACGAGATGCAGGAATGGGCG
                                                                                                                                                                                                                                                                                                                                                                          CAAAATCATAACATCCGCTCTAACCTAGAACGAATATTCGCAAAGGCTCCCGGAACCGTGG
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  CTCAGTGGACACCTAGACTTCAATGGTCGAGTCTTCTCGAATGATGTGCAGTATAACGTC
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This DNA sequence comprises a transdominant lethal mutant, designated TOMOV-ACIdImi, of the ACI gene of tomato mottle virus virus (TOMOV). It encodes an ACI protein (see AAW34325) that carries a mutation in its NTP-binding domains. The ACI gene (see also AAT93294) must be expressed for efficient replication of the two genomic components, DNA-A and DNA-B, of

genes - have increase mottle virus, tomato

Claim 11; Page 64-65; 132pp; English

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                                                                                                                                                                                                                  Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mottle virus, tomato yellow leaf curl virus or bean golden mosaic
                                                                                                                                                                                                                                                                                                                     WPI; 1997-526447/48.
P-PSDB; AAW34325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-APR-1997;
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Query Match
Best Local Similarity
Matches 1059; Conserv
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This DNA sequence comprises a transdominant lethal mutant, designated TOMOV-ACIAlm23, of the ACI gene of tomato mottle virus virus (TOMOV). I encodes an ACI protein (see AAW34326) that carries 2 mutations in an NT binding domain. The ACI gene (see also AAT93294) must be expressed for efficient replication of the two genomic components, DNA-A and DNA-B, o the bipartite TOMOV genome. The invention involves production of transgenic plants containing DNA comprising geminivirus ACI or CI wild-type or mutant sequences that negatively interfere in trans with geminiviral replication during infection. Such transgenic plants are resistant to viral infection. The ACI/CI genes are especially from TOMO'

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                                                                                                                                                                                                                                                                                                                                    Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mottle virus, tomato yellow leaf curl virus or bean golden mosaic
                                                                                                                                                                                                                                                               Claim 11; Page 67-69; 132pp; English.
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Best Local Sim:
Matches 1058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tomato yellow leaf curl virus or bean golden mosaic geminivirus (see AAT93282-93) and encode polypeptides (see AAW34324-35) that have mutations in the highly conserved DNA-nicking and/or the NTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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CCAGCAATCGTGCTTTGCAATCCTGGTGAGGGTGCCAGCTATAAAGAGTTTCTTAGACAAA
                                                         CAGAAAGATTGGCAATCAAATTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATC
                                                                                                                                                                                                                      GATAATTATTTCGGGACGGGTGACGCTGCGCCCGGATAGACCTGTAAGTATCATCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGCCCCCACCAAGAAATTTAGAGTTCAGTCAAAGAACTATTTCCTAACTTATCCCCAG
                                                                                                           ATTGATGACATCGCACCGCATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTGGGGGCC
                                                                                                                                                              CTCAGTGGACACCTAGACTTCAATGGTCGAGTCTTCTCGAATGATGTGCAGTATAACGTC
                                                                                                                                                                                                                                                         GATAATTATTTCGGGACGGGTGCAGCTGCGCGCCAGAGACCTGTAAGTATCATCGTC
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                                        CAGAAAGATTGGCAATCAAATTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATC
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97.7%;
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CACCAAAGAAATTTAGAGTTCAGTCAAAGAACTATTTCCTAACTTATCCCCAGTGCTCTC

Matches 1054; Query Match Best Local :

Conservative

0;

Pred. No. 0; 0; Mismatches Score 1040.8;

22; 2

Indels

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Gaps

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Local Similarity

96.1%; 98.0%;

Sequence

2602 BP; 671 A; 561 C; 586 G; 784

T; 0 U; 0 Other;

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ID AAT933
XX AAT9333
XX AAT933
XX 17-OCT
DT 17-OCT
DT 27-APR
XX Gemini
KW Gemini
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                                                    This genomic DNA sequence comprises a full-length A-component clone of tomato mottle virus (TOMOV), a geminivirus that has a bipartite genome comprising DNA-A and DNA-B. It was isolated from TOMOV infected Nicotiana benthamiana and tomato plant DNA by restriction digestion. The DNA-B component (see AAT93310) was also isolated. TOMOV DNA-A contains the ACI gene (see AAT9339) that must be expressed for efficient replication of DNA-A and DNA-B. The invention involves production of transgenic plants containing DNA comprising ACI or CI wild-type or mutant sequences that negatively interfere in trans with geminiviral replication during infection. Such transgenic plants are resistant to viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mottle virus, tomato yellow leaf curl virus or bean golden mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Geminivirus; ToMoV; AC1 gene; transdominant disease resistance; ss; cyclic; circular.
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27-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tomato mottle virus full-length A-component
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                           TCTATCAAGAGAGCACACAGGCAAGCCAAGAAACGGGCAATCAGAAGGCGCAAGGGT 1083
                                                                                                                      ATACAGGTCTCAAGAACTGGACTATCAAGAATGCGATCTTCATCACCCTCACAGCCCCCC
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P-PSDB;
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                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                     Tomato mottle virus; isolate Florida
                                                                                                                                                                                                                                                                                                Geminivirus; ToMoV-Acidlm; ACl gene; transdominant mutation; transgenic plant; disease resistance; ss; cyclic; circular.
                                                                                                       Claim 11; Page 60-62; 132pp; English
                                                                                                                                                                                                                 15-APR-1997;
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                                                                                                                                                                                                                                                                                                                                27-APR-1998
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                                                                                                                                                        1997-526447/48.
                                                                                                                                                                                 SEMINIS VEGETABLE SEEDS INC. WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                   AAW34324.
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                                                                                                                                                                                                                                                                                                                   virus AC1 mutant ToMoV-AC1dlm gene
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                                                                                                                                                                                                                                                            Location/Qualifiers
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Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mottle virus, tomato yellow leaf curl virus or bean golden mosaic

This DNA sequence comprises a transdominant lethal mutant, designated TOMOV-ACIdlm, of the ACI gene of tomato mottle virus virus (TOMOV). It encodes an ACI protein (see AAW34324) that carries mutations in its NTP-binding domains. The ACI gene (see also AAT93294) must be expressed for efficient replication of the two genomic components, DNA-A and DNA-B, of the bipartite TOMOV genome. The invention involves production of transgenic plants containing DNA comprising geminivirus ACI or CI wild-type or mutant sequences that negatively interfere in trans with geminiviral replication during infection. Such transgenic plants are resistant to viral infection. The ACI/CI genes are especially from TOMOV, tomato yellow lasf curl virus or bean golden mosaic geminivirus (see AAT93282-93) and encode polypeptides (see AAW34324-35) that have mutations in the highly conserved DNA-nicking and/or the NTP-binding

Sequence 1169 BP; 363 A; 281 C; 255 G; 270 T; 0 U; 0 Other;

Query Match Best Local

Similarity

95.9%;

DB 2;

Length 1169

밁 Ś 밁 5 B S Matches 1055; 164 121 104 61 44 \_ AAGAAATTCATCAAAATTTGCAGAGAGCTTCATGAAAATGGGGAACCTCATCTCCATGTG 180 TGCTCTATCTAAAGAAGAAGAACCTTTCCCCAATTACAAAACCTAAATACCCCCAGTCAAC ATGCCCCCACCAAAGAAATTTAGAGTTCAGTCAAAGAACTATTTCCTAACTTATCCCCAG ATGCCCCCACCAAAGAAATTTAGAGTTCAGTCAAAGAACTATTTCCTCACTTATCCACAG TGCTCTTTGTCTAAAGAAGAAGCACTTTCCCCAATTACAAAACCTAAATACCCCAGTCAAT Conservative Score 1038.2; Pred. No. 0; 0; Mismatches 0, 28; Indels 0, Gaps 163 120 103 60 0

RESULT 5 AAT93282

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                                        164
                                                                        104
        224
                                                        121
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Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato motile virus, tomato yellow leaf curl virus or bean golden mosaic
                                                                                                 WPI; 1997-526447/48.
P-PSDB; AAW34327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Geminivirus; ToMoV-Ac1dlm23; AC1 gene; transdominant mutation;
                                                                                                                                                                                                                                                                                                                             15-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                     WO9739110-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomato mottle
                                                                                                                                                                                                              (SEMI-) SEMINIS VEGETABLE SEEDS INC (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transgenic plant; disease resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mottle virus
                                                                                                                                                                 Luu HT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virus; isolate Florida
                                                                                                                                                                                                                                                                                  96US-0015517P
                                                                                                                                                                                                                                                                                                                             97WO-US006300
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                   Hanson SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC1 mutant gene
                                                                                                                                                                   Maxwell DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ss; cyclic;
                                                                                                                                                                   Ahlquist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           circular
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Claim 11; Page 72-73; 132pp; English.

This DNA sequence comprises a mutated AC1 gene of tomato mottle virus (TOMOV). It carries an inserted 4-base Sau3A site that shifts the AC1 gene translation reading frame resulting in the expression of a truncated AC1 protein (see AAW3427). The AC1 gene (see also AAT93294) must be expressed for efficient replication of the two genomic components, DNA-A and DNA-B, of the bipartite TOMOV genome. The invention involves production of transgenic plants containing DNA comprising geminivirus AC1 or C1 wild-type or mutant sequences that negatively interfere in trans with geminiviral replication during infection. Such transgenic plants are resistant to viral infection. The AC1/C1 genes are especially from TOMOV, tomato yellow lasf curl virus or bean golden mosaic geminivirus (see AAT93282-93) and encode polypeptides (see AAW34324-35) that have mutations in the highly conserved DNA-nicking and/or the NTP-binding

1166 BP; 361 A; 277 C; 260 G; 268 T; 0 U; 0 Other;

Matches 1061; Local Similarity AAGAAATTCATCAAAATTTGCAGAGAGATCATGAAAATGGGGAACCTCATCTCCATGTG TGCTCTTTGTCTAAAGAAGAAGCACTTTCCCAATTACAAAACCTAAATACCCCAGTCAAT TGCTCTCTATCTAAAGAAGAAGCACTTTCCCCAATTACAAAACCTAAATACCCCAGTCAAC ATGCCCCCAACCAAAGAAATTTAGAGTTCAGTCAAAGAACTATTTCCTAACTTATCCCCCAG CTTGTTCAGTTCGAAGGAAAGTACCAGTGCACGAATAACAGATTCTTCGACCTGGTCTCC CTTGTTCAGTTCGAAGGTAAGTACCAATGCACGAATAACAGATTCTTCGACCTGGTCTCC ATGCCCCCACCAAAGAATTTAGAGTTCAGTCAAAGAACTATTTCCTCACTTATCCACAG Conservative 95.5%; 97.6%; 0; Score 1033.8; Pred. No. 0; Mismatches DB 2; 22; Indels Length 1166; 4. Gaps 180 163 120 60 240 223 103

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AAT93286
ID AATS
XX
AC AATS
XC TOT 17-C
DT 27-J
XX
XX
CHART TOTA
XX
CHAR
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                                                                                                         17-OCT-2003
27-APR-1998
                                                                                                                                                                                                                                           AAT93286 standard; DNA; 1246 BP
  Geminivirus;
                                                    Tomato mottle virus AC1-AC2-AC3 DNA
                                                                                                                                                                                    AAT93286;
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ToMoV-Acidlm; AC1 gene; transdominant mutation;
                                                                                                         (revised)
(first entry)
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WPI; 1997-526447/48.
                                                                                                                             Stout JT,
                                                                                                                                                   16-APR-1996;
                                                                                                                                                            15-APR-1997;
                                                                                                                                                                                     Tomato mottle virus; isolate Florida
                                                                                                                                                                                               transgenic plant; disease resistance; ss; cyclic; circular
                                                                                                                                      (SEMI-) SEMINIS VEGETABLE SEEDS INC
                                                                                                                             Luu HT,
                                                                                                                                                   96US-0015517P
                                                                                                                                                            97WO-US006300
                                                                                                                             Hanson SF, Maxwell DP,
                                                                                                                                           INC.
                                                                                                                              Ahlquist
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Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato motile virus, tomato yellow leaf curl virus or bean golden mosaic

Claim 11; Page 75; 132pp; English

This DNA sequence comprises the complete AC2 and AC3 coding sequences and CC the C-terminal two-thirds of the AC1 open reading frame (see also AT93924) of tomato mosaic virus (TOMOV). It was obtained by ligating a BamHI-HindIII fragment of a binary plasmid composed of a dimer of the full-length, infectious TOMOV A-component with BamHI-HindIII-digested pJTS222, inserting a BamHI-HindIII ragment of this construct into pBluescript II KS+, and digesting with BgII and SphI. The AC1 gene must be expressed for efficient replication of the two genomic components, DNA can be appeared for efficient replication of the two genomic components, DNA can be constructed by a fine bipartite TOMOV genome. The invention involves production of transgenic plants containing DNA comprising geminivirus AC1 or C1 wild-type or mutant sequences that negatively interfere in transfer with geminiviral replication during infection. Such transgenic plants are resistant to viral infection. The AC1/C1 genes are especially from TOMOV, tomato yellow leaf curl virus or bean golden mosaic geminivirus (see AAT93282-93) and encode polypeptides (see AAW34324-35) that have mutations in the highly conserved DNA-nicking and/or the NTP-binding componence.

Sequence 1246 BP; 393 A; 264 C; 284 G; 305 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                   Query Match
Best Local !
                                                                                               181
 301
                       661
                                               241
                                                                       601
                                                                                                                    541
                                                                                                                                            121
                                                                                                                                                                  481
                                                                                                                                                                                                                  421
                                                                                                                                                                                                                                                               361 AGATCTGCCAGAGGAGGCCAGCAGTCTGCTAATGATTCATATGCGAAAGCATTAAATGCA
                                                                                                                                                                                                                                                                                       710;
                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                    Similarity
             GATAATTATTTCGGGACGGGTGACGCTGCGCCGCCGCTAGACTCGTTAAGTATCATCGTC
                                                                                                                                                         CAAAATCATAACATCCGCTCTAACCTAGAACGAATATTCGCAAAGGCTCCGGAACCGTGG
                                                                                                                                                                                          GGTTCGGTTCAATCTGCCTTAGCGGTTCTAAGGGAAGAACAACCAAAAGATTTTGTATTA
                                                                                                          GTTCCTCCATTTCAAGTCTCTTCTTCACTAACGTTCCTGACGAGATGCAGGAATGGGCG
                                                                                                                                            CAAAATCATAACATCCGCTCTAACCTAGAACGAATATTCGCAAAGGCTCCGGAACCGTGG
 GAGGGTGATTCAAGAACAGGGAAGACGATGTGGGCACGTGCGTTAGGCCCCACATAACTAT
                                                                                               GTTCCTCCATTTCAAGTCTCTTTTCACTAACGTTCCTGACGAGATGCAGGAATGGGCG
                                                                                                                                                                                                                                          AGATCTGCCAGAGGAGGCCAGCAGTCTGCTAATGATTCATATGCGAAAGCGTTAAATGCA
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                  64.8%;
98.2%;
                                                                                                                                                                                                                                                                                       <u>,</u>
                                                                                                                                                                                                                                                                                                   Score 702.2; DB 2;
Pred. No. 1.7e-212;
                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                              Length 1246;
                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                        Gaps
                                                300
                                                                       660
                                                                                                240
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                                                                                                                                             180
                                                                                                                                                                   540
                                                                                                                                                                                           120
                                                                                                                                                                                                                   480
                                                                                                                                                                                                                                          60
                                                                                                                                                                                                                                                                                         0
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Indels Length 1183;

0;

Gaps

0

0 Other

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RESULT 8
AAT93314
ID AAT9
XX AAT9
AC AAT9
XX AAT9
XX Gemi
XW Gemi
XX HO97
XX 15-A
XX W097
XX 16-A
XX W15-A
XX WPI;
DR WPI;
DR PPE Trar
PT Trar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
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                                                                       Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mottle virus, tomato yellow leaf curl virus or bean golden mosaic
                                                         geminivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-2003
27-APR-1998
                   Example 5; Page 100-102; 132pp; English
                                                                                                                                                                       WPI; 1997-526447/48.
                                                                                                                                                                                                                                                                                                       16-APR-1996;
                                                                                                                                                                                                                                                                                                                                         15-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                    WO9739110-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Geminivirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT93314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT93314 standard; DNA; 1183
                                                                                                                                                                                                                                              (SEMI-) SEMINIS VEGETABLE SEEDS INC. (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                golden mosaic virus; type II isolate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       721
                                                                                                                                                     AAW34338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  irus; BGMV; C1 gene; transdominant mutation; transgenic
resistance; ss; cyclic; circular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCCCCCTTATCAAGAGAGCACACAGGCAAGCCAAGAAACGGGCAATCAGAAGGCGCAG 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAGAAAATACAGGTCTCAAGAACTGGACTATCAAGAATGCGATCTTCATCACCCTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTGATGACATCGCACCGCATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTGGGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTGATGACATCGCACCGCATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTAGGGGCC
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                                                                                                                                                                                                           Luu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mosaic geminivirus C1 open reading
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(first en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                           Hanson SF, Maxwell DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
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                                                                     or bean golden mosaic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1183 BP; 372 A; 276 C; 248
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                                                                                                                                          GTTCCTCCATTTCAAGTCTCTTTCTTTCACTAACGTTCCTGACGAGATGCAGGAATGGGCG
                                                                                                                                                                                                                                                                                                                                                                   CAAAATCATAACATCCGCTCTAACCTAGAACGAATATTCGCAAAGGCTCCGGAACCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTTCGGTTCAATCTGCCTTAGCGGTTCTAAGGGAAGAACAACCAAAAGATTTTGTATTA
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 ATTGATGACATCGCACCGCATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTGGGGGCC
                                   TTGAGCGGTCATTTGGACTTTAATTCACGTGTCTATTCCAACGCAGTGGAATACAACGTC
                                                                       CTCAGTGGACACCTAGACTTCAATGGTCGAGTCTTCTCGAATGATGTGCAGTATAACGTC
                                                                                                                GAAGGTGATTCACGAACCGGAAAGACAATGTGGGCTCGTGCATTAGGACCACATAATTAT
                                                                                                                                                                                         GACGACTATTTCGGAAGGGGTTCCGCTGCGCGGCCGGAAAGACCTATTAGTATCATCGTC
                                                                                                                                                                                                                                                                GTTCCTCCATTTCCGTTGTCATCATTCATCAATGTTCCGGTTGTTATGCAAGAATGGGTT
                                                                                                                                                                                                                                                                                                                                           CAACATCACAACATCCGTTCTAATCTCGAACGGATCTTCGTCAAAGTGCCGGAACCATGG
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77.9%;
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Pred. No. 1.
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ches 238;
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                The present sequence is a 35S-rep gene cassette comprising the rep gene of bean golden mosaic virus (BGNV)-GA cloned downstream of the CaNV 35S promoter and an alfalfa mosaic virus (AMV) leader sequence. The sequence was integrated into pBSII-KS+ to produce a rep gene expression vector. DNA-nicking domain mutations may be incorporated into rep gene to produce a genetic construct that acts as a trans-dominant inhibitor of geminiviral replication. When expressed in a plant cell, this inhibitor is able to dramatically reduce replication of geminivirus. Genetic constructs that include sequences containing a portion of the ac3 gene in addition to the trans-dominant inhibitor exhibit increased efficiency and broadened specificity of inhibition of geminivirus replication. Geminiviruses are one of the greatest constraints on production of important crops, including cassava, beans, compass, peppers, tomatoes and cotton. The effects of the virus can be overcome by using the genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Geminivirus; DNA-A; geminivirus replication inhibition; ac3 gene; transgenic plant; antiviral; gene therapy; bean golden mosaic vir BGMV; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CaMV;
                                                                                                                                                                                                                                                                                                                                                                                             Genetic construct comprising a mutant geminiviral rep gene, producing a plant resistant to geminiviral infection.
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RESULT 10
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Best Local S
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                                                                                                                                                                                                                                                                             The present sequence is pTrep23deltaE/CX. It contains a mutated geminivirus rep gene sequence. Genetic constructs containing DNA-nicking domain mutants in the rep gene may be used as trans-dominant inhibitors of geminiviral replication. When expressed in a plant cell, these inhibitors are able to dramatically reduce replication of geminivirus. Genetic constructs that include sequences containing a portion of the acl gene in addition to the trans-dominant inhibitor exhibit increased efficiency and broadened specificity of inhibition of geminiviral replication. Geminiviruses are one production of important crops, including cassava, beans, cowpeas, peppers, tomatoes and cotton. The effects of the virus can be overcome by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetic construct comprising a mutant geminiviral rep gene, useful for producing a plant resistant to geminiviral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Geminivirus; DNA-A; geminivirus replication inhibition; transgenic plant; antiviral; gene therapy; ds.
                                                                                                                                                                                                                                         Sequence 1894 BP; 604 A; 421 C; 388 G; 481 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Col 19-22; 14pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-610861/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maxwell
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                                                    AAGAAATTCATCAAAATTTGCAGAGAGCTTCATGAAAATGGGGAACCTCATCTCCATGTG
                                                                             TGCCCTATACCGAAAGAAGATTCTTTCGCAACTTCAGAAGATTCATACAGCCACGAAT
                                                                                                        TGCTCTCTATCTAAAGAAGAAGCACTTTCCCAATTACAAAACCTAAATACCCCAGTCAAC
                                                                                                                                                   ATGCCCCCACCAAGAAATTTAGAGTTCAGTCAAAGAACTATTTCCTAACTTATCCCCAG
 CTTGTTCAGTTCGAAGGTAAGTACCAATGCACGAATAACAGATTCTTCGACCTGGTCTCC
                        AAAAAATTCATCAAAGTCTGTGAGGAACGTCACGAGAATGGTGAACCTCATCTTCATGCG
                                                                                                                                  ATGCCACCACCTCAAAGATTTAGAGTTCAGTCGAAAAACTATTTCCTCACTTATCCTCGT
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                                                                                                                                                                                     Conservative
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77.9%;
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Geminivirus; DNA-A; geminivirus replication inhibition; ac3 transgenic plant; antiviral; gene therapy; ds.
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Matches 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rep gene sequence. Genetic constructs containing DNA-nicking domain mutants in the rep gene may be used as trans-dominant inhibitors of geminiviral replication. When expressed in a plant cell, these inhibitors are able to dramatically reduce replication of geminivirus. Genetic constructs that include sequences containing a portion of the ac3 gene in addition to the trans-dominant inhibitor exhibit increased efficiency and broadened specificity of inhibition of geminivirus are one of the greatest constraints on production of Geminiviruses are one of the greatest constraints on production of important crops, including cassava, beans, cowpeas, peppers, tomatoes and cotton. The effects of the virus can be overcome by using the genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2072 BP; 661 A; 467 C; 421 G; 523 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Col 17-20; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetic construct comprising a mutant geminiviral rep gene, useful producing a plant resistant to geminiviral infection.
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CAAAATCATAACATCCGCTCTAACCTAGAACGAATATTCGCAAAGGCTCCGGAACCGTGG
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Pred. No. 1.8e-210;
0; Mismatches 238;
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                                                                                          (SEMI-) SEMINIS VEGETABLE SEEDS INC. (WISC ) WISCONSIN ALUMNI RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                   WO9739110-A1
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27-APR-1998
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutangenes - have increased resistance to geminivirus infection e.g. tomato genes - towasto yellow leaf curl virus or bean golden mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-526447/48
P-PSDB; AAW34332.
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                                                                                                                                   CAAAATCATAACATCCGCTCTAACCTAGAACGAATATTCGCAAAGGCTCCGGAACCGTGG
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                                             GTTCCTCCATTTCCGTTGTCATCATTCCGCAATGTTCCGGTTGTTATGCAAGAATGGGTT
                                                                                                             CAACATCACAACATCCGTTCTAATCTCGAACGGATCTTCGTCAAAGTGCCGGAACCATGG
                                                                                                                                                                             GATTCAATTGAATCTGCCTTGACAATATTGAAGGAAGAACAACCGAAAGATTACGTCCTT
                                                                                                                                                                                                            GGTTCGGTTCAATCTGCCTTAGCGGTTCTAAGGGAAGAACAACCAAAAGATTTTGTATTA
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RESULT 13
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ID AAA94
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Cauliflower mosaic virus.
Alfalfa mosaic virus
The present sequence is pTrepN, a vector containing a CaMV-35S promoter-driven rep gene derived from bean golden mosaic virus (BGNV)-GA. Sitedirected mutagenesis was used to engineer an Ncol site in the start codo of the rep gene to facilitate cloning of DNA-nicking domain mutants. The resulting genetic constructs act as trans-dominant inhibitors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Geminivirus; DNA-A; geminivirus replication inhibition; ac3 gene; transgenic plant; antiviral; gene therapy; bean golden mosaic virus; BGMV; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CAMV; ds.
                                                                                                                                                                                                                                       Genetic construct comprising a mutant geminiviral rep producing a plant resistant to geminiviral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-APR-1998;
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  ATTGATGACATAAGCCCCAATTATTTGAAGTTAAAGCACTGGAAAGAACTAATTGGGGCA
                                             ATTGATGACATCGCACCGCATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTGGGGGCC
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77.8%;
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Pred. No. 5.1e-210;
0; Mismatches 239;
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CAGAAAGATTGGCAATCAAATTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATC

Query Match Best Local Similarity

63.8**%**; 78.4**%**;

Score 691.2; DB 2; Pred. No. 4.9e-209;

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Length 1062

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ID AAT93
XX AT93
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                                                    This DNA sequence comprises construct BGAC221 that codes for a transdominant lethal mutant (see AAW3433) of the C1 protein (see AAW34338) of bean golden mosaic virus (BGMV). It was obtained by Kunkel mutagenesis of the wild-type C1 gene (see AAT93314). C1 is required for replication. The invention involves production of transgenic plants containing DNA comprising geminivirus C1 or AC1 wild-type or mutant sequences that negatively interfere in trans with geminiviral replication during infection. Such transgenic plants are resistant to viral infection. The AC1/C1 genes are especially from BGMV, tomato mottle virus or tomato yellow leaf curl virus (see AAF93282-93) and encode polypeptides (see AAW34324-35) that have mutations in the highly conserved DNA-nicking and/or the NTP-binding domains. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mottle virus, tomato yellow leaf curl virus or bean golden mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; Page 107-109; 132pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stout JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-1996;
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                                                                                                     GCAGAAAATACAGGTCTCAAGAACTGGACTATCAAGAATGCGATCTTCATCACCCTCACA
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                                                                                                                                                            CCATCAATCGTGTTGTGCAATCCAGGTGAGGGTTCCAGTTATAAAGACTTCCTCGACAAA
                                                                                                                                                                                                                                           CAAAAGGACTGGCAATCTAACTGTAAATATGGAAAGCCGGTTCAAATTAAAGGAAGAATA
                                                                                                                                                                                                                                                                                                                           ATTGATGACATAAGCCCCAATTATTTGAAGTTAAAGCACTGGAAAGAACTAATTGGGGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This DNA sequence comprises construct BGAC228 that codes for a transdominant lethal mutant (see AAW34334) of the C1 protein (see AAW34338) of bean golden mosaic virus (BGMV). It was obtained by Kunkel mutagenesis of the wild-type C1 gene (see AAT93314). C1 is required for replication. The invention involves production of transgenic plants containing DNA comprising geminivirus C1 or AC1 wild-type or mutant sequences that negatively interfere in trans with geminiviral replication during infection. Such transgenic plants are resistant to viral infection. The AC1/C1 genes are especially from BGMV, tomato mottle virus or tomato yellow leaf curl virus (see AAT93382-93) and encode polypeptides (see AAW34324-35) that have mutations in the highly conserved DNA-nicking and/or the NTP-binding domains. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mottle virus, tomato yellow leaf curl virus or bean golden mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1062 BP; 338 A; 247 C; 218 G; 259 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-526447/48.
P-PSDB; AAW34334.
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27-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13;
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  AAAAAATTCATCAAAGTCTGTGAGGAACGTCACGAGAATGGTGAACCTCATCTTCATGCG
                                                     AAGAAATTCATCAAAATTTGCAGAGAGCTTCATGAAAATGGGGAACCTCATCTCCATGTG
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Pred. No. 4.9e-209;
0; Mismatches 228;
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	1021 GCCCCCTCTATCAAGAGAGAGACACAGGCAAGCCAA 1056 	
1020 1020	961 GCAGAAAATACAGGTCTCAAGAACTGGACTATCAAGAATGCGATCTTCATCACCCCTCACA	
960	901 CCAGCAATCGTGCTTTGCAATCCTGGTGAGGGTGCCAGCTATAAAGAGTTCTTAGACAAA 	
900	841 CAGAAAGATTGGCAATCAAATTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATC 	
840 840	781 ATTGATGACATCGCACCGCATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTGGGGGCC	
780 780	721 CTCAGTGGACACCTAGACTTCAATGGTCGAGTCTTCTCGAATGATGTGCAGTATAACGTC	
720 720	661 GAGGGTGATTCAAGAACAGGGAAGACGATGTGGGCGCGTGCGT	
660	601 GATAATTATTICGGGACGGGTGACGCTGCGCCGGATAGACCTGTAAGTATCATCGTC	
600	541 GTTCCTCCATTTCAAGTCTCTTTTCACTAACGTTCCTGACGAGATGCAGGAATGGGCG 	
540 540	481 CAAAATCATAACATCCGCTCTAACCTAGAACGAATATTCGCAAAGGCTCCGGGAACCGTGG 	
480 480	421 GGTTCGGTTCAATCTGCCTTAGCGGTTCTAAGGGAAGAACAACCAAAGATTTTGTATTA	
420 420	361 AGATCTGCCAGAGGAGGCCAGCAGTCTGCTAATGATTCATATGCGAAAGCATTAAATGCA 	
360 360	301 AAATCATACATCGACAAGGACGGAGATACAATCGAATGGGGAGATTTCCAAATCGACGGC 	
300	241 CCAACCCGGTCAGCACATTTCCATCCGAATATTCAGGGAGCTAAATCGAGCTCCGACGTC	
240	181 CTTGTTCAGTTCGAAGGTAAGTACCAATGCACGAATAACAGATTCTTCGACCTGGTCTCC	

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Search completed: December 4, 2004, 13:50:53 Job time : 608 secs

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Listing first 45 summaries
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Match
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/ETUS_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfīles1.seq:*
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## ALIGNMENTS

, NAME/KEY: CDS
L ISOLATE: Florida
ORGANISM: Tomato Mottle Gemini Virus
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; ANTI-SENSE: NO
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DEDNESS:
nucleic acio
; LENGTH: 1162 base pairs
; SEQUENCE CHARACTERISTICS:
; INFORMATION FOR SEQ ID NO: 1:
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; TELEPHONE: 312-616-5400
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; NAME: Mueller, Lisa V
; CLASSIFICATION: 800
; APPLICATION NUMBER: US/08/838,151A
LICATION DATA:
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; OPERATING SYSTEM: PC-DOS/MS-DOS
; COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
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Chicago
o Prudential Plaza, Suite 4700
: ADDRESSEE: Dressler, Rockey, Milnamow & Katz
· CORREGOONDENCE ADDREGO:
INVENTION: C
OF INVENTION:
CANT: Hanson, Steve
Ahlquist,
; APPLICANT: Maxwell, Douglas
Luu, Hang T
APPLICANT: Stout, John T
GENERAL INFORMATION:
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Semience 1. Application US/08838151A
US-08-838-151A-1

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; IOCATION: 44..1127
; PUBLICATION IMFORMATION:
AUTHORS: Gilbertson, RL
; AUTHORS: Hidayat, SH
; AUTHORS: Paplomatas, EJ
AUTHORS: Paplomatas, EJ
AUTHORS: Rojas, MR
; AUTHORS: Hou, YM
AUTHORS: Hou, YM
AUTHORS: Hou To the infectious
TITLE: Pseudorecombination between the infectious
TITLE: cloned DNA components of tomato mottle and bea
TITLE: dwarf mosaic geminiviruses.
JOURNAL: Jour. General Virol.
VOLUME: 74
PAGES: 23-31
DATE: 1993
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CAAAATCATAACATCCGCTCTAACCTAGAACGAATATTCGCAAAGGCTCCGGAACCGTGG
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MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Tomato Mottle Gemini Virus STRAIN: Florida	INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 1169 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: circular	CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION: NAME: Mueller, Lisa V REGISTRATION NUMBER: 38,978 REFERENCE/DOCKET NUMBER: SVS3801P0260 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-616-5400 TELEPHONE: 312-616-5400	COUNTRY: U.S.A.  ZIP: 60601  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: IBM FC compatible  OPERATING SYSTEM: PC_DOS/MS-DOS  SOFTWARE: PatentIn Release #1.0, Version #1.30  CURRENT APPLICATION DATA:  APPLICATION NUMBER: US/08/838,151A  FILING DATE:	APPLICANT: Aniquist, Paul APPLICANT: Hanson, Steve TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus TITLE OF INVENTION: Genes NUMBER OF SEQUENCES: 63 CORRESPONDENCES Dressler, Rockey, Milnamow & Katz ADDRESSE: Dressler, Rockey, Milnamow & Katz STREET: Two Prudential Plaza, Suite 4700 CITY: Chicago STATE: Illinois	2 308-151A-5 308-5, Application to it No. 6291743 3RAL INFORMATION: 3PLICANT: Stout, Joh PLICANT: Luu, Hang PLICANT: Maxwell, I	1081 GGT 1083     1124 GGT 1126	1021 GCCCCCTCTATCAAGAGAGACACAGGCAAGCCAAGAAACGGGCAATCAGAAGGCGCAG 1080	961 GCAGAAAATACAGGTCTCAAGAACTGGACTATCAAGAATGCGATCTTCATCACCCTCACA 1020 	901 CCAGCAATCGTGCTTTGCAATCCTGGTGAGGGTGCCAGCTATAAAGAGTTCTTAGACAAA 960 	841 CAGAAAGATTGGCAATCAAATTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATC 900 	781 ATTGATGACATCGCACCGCATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTGGGGGCC 840

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                                                                                                                                                                                                                                                                                                    GATAATTATTTCGGGACGGGTGACGCTGCGCCGCCGGATAGACCTGTAAGTATCATCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                       CAAAATCATAACATCCGCTCTAACCCTAGAACGAATATTCGCAAAAGGCTCCCGGAACCGTGG
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                                                                       CAGAAAGATTGGCAATCAAATTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATC
                                                                                                             ATTGATGACATCGCACCGCATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTAGGGGCC
                                                                                                                                                                                        CTCAGTGGACACCTAGACTTCAATGGTCGAGTCTTCTCGAATGATGTTGCAGTATAACGTC
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CCAGCAATCGTGCTTTGCAATCCTGGTGAGGGTGCCAGCTATAAAGAGTTCTTAGACAAA
                                                        CAGAAAGATTGGCAATCAAATTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATC
                                                                                                                                        ATTGATGACATCGCACCGCATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTGGGGGCC
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Pred. No. 0;
0; Mismatches
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US-08-838-151A-7
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                                                                                                             US-08-838-151A-7
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APPLICANT: Stout,
APPLICANT: Luu, Hai
APPLICANT: Maxwell
APPLICANT: Ahlquis
                                           Query Match
Best Local Similarity
Matches 1058; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08838151A Patent No. 6291743
                                                                                                                                                                                                                                                                                                                  TELEPHONE: 312-616-5400
TELEPAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1169 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
ATTORNEY AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3
TELECOMMUNICATION:
                                                                                                                                                                                                      MOLECULE TYPE: DNI
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                         FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: IIII....
COUNTRY: U.S.A.
COUNTRY: 60601
TIP: 60601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: circular
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                                                                                                                                                                                         ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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             ATGCCCCCACCAAGAAATTTTAGAGTTCAGTCAAAGAACTATTTCCTAACTTATCCCCAG
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Two Prudential Plaza, Suite 4700
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Maxwell, Douglas
Ahlquist, Paul
                                             Conservative
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Luu, Hang T
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97.7%;
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                                           Score 1043; I
Pred. No. 0;
0; Mismatches
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ATGCCCCCACCAAAGAAATTTAGAGTTCAGTCAAAGAACTATTTCCTCACTTATCCACAG

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEPHONE: 312-616-5400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2602 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Gemin:
STRAIN: Florida
US-08-838-151A-17
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US-08-838-151A-17/c
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION NUMBER: US/08/838,151A
FILING DATE:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Pl
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
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CITY: Chicago
STATE: Illinois
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                    GGTCAGCACATTTCCATCCGAATATTCCAGGGAGCTAAATCGAGCTCCGACGTCAAATCAT
                                                                                                                                                                       TCATCAAAATTTGCAGAGAGCTTCATGAAAATGGGGGAACCTCATCTCCATGTGCTTGTTC
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GGTCAGCACATTTCCATCCGAATATTCAGGGAGCTAAATCGAGCTCCGACGTCAAATCGT
                                                                      AGTTCGAAGGAAAGTACCAGTGCACGAATAACAGATTCTTCGACCTGGTCTCCCCAACCC
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98.0%;
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Pred. No. 0;
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RESULT 5
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                                                                                                   GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Luu, Hang T

APPLICANT: Maxwell, Douglas

APPLICANT: Matwell, Douglas

APPLICANT: Ahlquist, Paul

APPLICANT: Hanson, Steve

TITLE OF INVENTION: Transgenic Plants Expressing

TITLE OF INVENTION: Genes

NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
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ATTORNEY/AGENT INFORMATION:
NAME: MUBLIC: Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3;
TELECOMMUNICATION : 1160-5400
TELEPHONE: 312-616-5400
TELEPAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1169 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 96.0%;
Best Local Similarity 97.5%;
Matches 1056; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 44..1127
PUBLICATION INFORMATION:
AUTHORS: Gilbertson, RL et al.
TITLE: Pseudorecombination between the infectious
TITLE: cloned DNA components of tomato mottle and bean
TITLE: dwarf mosaic geminivirus.
JOURNAL: Journal of General Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
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HYPOTHETICAL:
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VOLUME: 74
PAGES: 23-31
DATE: 1993
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STRANDEDNESS: single
TOPOLOGY: circular
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Maxwell, Douglas
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
NUMBER OF SEQUENCES: 63
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 312-616-5400
TELEPAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1166 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Geminivirus
INDIVIDUAL ISOLATE: Florida
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM_PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
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LOCATION:
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STRANDEDNESS: single
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                       GTGGGTTCCTCCATTTCAAGTCTCTTTCTTTCACTAACGTTCCTGACGAGATGCAGGAATG
                                                                            ATTACAAAATCATAACATCCGCTCTAACCTAGAACGAATATTCGCAAAGGCTCCGGAACC
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97.6%;
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Indels Length 1166;

4. Gaps

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US-08-838-151A-15; Sequence 15, Application US/08838151A; Patent No. 6291743; GENERAL INFORMATION:
                                                                                                                                  ADDRESSEE: Dressler, Rockey, Milnamow & Katz STREET: Two Prudential Plaza, Suite 4700 CITY: Chicago STATE: Illinois COUNTRY: U.S.A. ZIP: 60601 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPACTING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838
FILING DATE:
CLASSIFICATION: 800
ATTORNBY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genees
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
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                                                                                                                       US/08/838,151A
                   SVS3801P0260
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; DATE: 1993
US-08-838-151A-15
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Best Local Similarity
Matches 710; Conserv
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TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle G
STRAIN: Florida
PUBLICATION INFORMATION:
AUTHORS: Gilbertson, RL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS: Hidayat, SH
AUTHORS: Paplomatas, EJ
AUTHORS: Rojas, MR
AUTHORS: Rojas, MR
AUTHORS: Hou, YM
AUTHORS: Maxwell, DP
TITLE: Pseudorecombination between the infectious
TITLE: cloned DNA components of tomato mottle and be
TITLE: dwarf mosaic geminiviruses.
JOURNAL: Journal of General Virology
VOLUME: 74
PACES: 73-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: cir
MOLECULE TYPE:
HYPOTHETICAL: N
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STRANDEDNESS: sing
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                       CCAGCAATCGTGCTTTGCAATCCTGGTGAGGGTGCCAGCTATAAAGAGTTCTTAGACAAA
                                                                                                                                                                                                                                                                                                     AGTTCGGTTCAATCTGCCTTAGCAGTTCTAAGGGAAGAACAACCAAAAGATTTTGTATTA
                                                                                          CAGAAAGATTGGCAATCAAATTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATC
                                                                                                                                                           ATTGATGACATCGCACCGCATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTGGGGGCC
                                                                                                                                                                                                            CTCAGTGGACACCTAGACTTCAATGGTCGAGTCTTCTCGAATGATGTGCAGTATAACGTC
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                                                                    CAGAAAGATTGGCAATCAAATTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATC
                                                                                                                                         ATTGATGACATCGCACCGCATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTAGGGGCC
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RESULT 7

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RESULT 8
US-08-838-151A-43
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INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
SEQUENCE 1183 base pairs
LENGTH: 1183 base pairs
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Patent No. 6291743
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PM PC POS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Va
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genc
                                                                LOCATION:
PUBLICATION:
AUTHORS:
                                                                                                                               FEATURE:
NAME/KEY:
                                                                                                                                                                         HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Geminivirus
STRAIN: Type II Isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants
TITLE OF INVENTION: Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                  AUTHORS:
AUTHORS:
AUTHORS:
                                                                                                                                                                 INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Illinois COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
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Two Prudential Plaza, Suite 4700
Morales, FJ
Ahlquist, P
Loniello, AO
                                               Gilbertson, RL
Hanson, SF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stout, John T
Luu, Hang T
                                                                                                INFORMATION:
                                                                                                                                 CDS
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                                                                                                                                                               Guatemala
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                                                                                                                                                                                                                                                                                                                                                                                                                                          38,978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.30
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISSUE: 321-3
PAGES: 321-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS:
TITLE: B
TITLE: I
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VOLUME:
                                 781
                                                              781
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   CAGAAAGATTGGCAATCAAATTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATC
                                                                ATTGATGACATCGCACCGCATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTGGGGGCC
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                                                                                                  TTGAGCGGTCATTTGGACTTTAATTCACGTGTCTATTCCAACGCAGTGGAATACAACGTC
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Bean Golden Mosaic Geminivirus Type II
Isolates from the Dominican Republic and
Guatemala: Nucleotide Sequences, Infectious
Pseudorecombinants, and Phylogenetic Relationships
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77.9%;
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Pred. No. 1.3e-218;
0; Mismatches 238;
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US-09-065-999-5
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                                                                                                                                                                                                                                                                                                                                        TELEPAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1651 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09065999
Patent No. 6118048
GENERAL INFORMATION:
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                         Matches 839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: FR FC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 9602
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hanson, Stephen F.

APPLICANT: Maxwell, Douglas P.

TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL

TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                     AAGAAATTCATCAAAATTTGCAGAGAGCTTCATGAAAATGGGGGAACCTCATCTCCCATGTG
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AAAAATTCATCAAAGTCTGTGAGGAACGTCACGAGAATGGTGAACCTCATCTTCATGCG
                                                                       TGCCCTATACCGAAAGAAGAAGTTCTTTCGCAACTTCAGAAGATTCATACAGCCACGAAT 588
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Pred. No. 1.6e-218;
0; Mismatches 238;
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             Sequence 8, Application US/09065999
Patent No. 6118048
GENERAL INFORMATION:
APPLICANT: Hanson, Stephen F.
APPLICANT: Maxwell, Douglas P.
TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE 1
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 9602
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genom:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
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OTTY: Madison
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ZIP: 53701-2113
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                                                                             CAAAATCATAACATCCGCTCTAACCTAGAACGAATATTCGCAAAGGCTCCGGAACCGTGG
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Pred. No. 1.7e-218;
0; Mismatches 238;
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Patent No. 6118048
GENERAL INFORMATION:
        TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2072 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                               ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPES Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTIN Release #1.0, V
CURRENT APPLICATION DATA:
                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 9602
TELECOMMUNICATION INFORMATION:
TELEPIONE: 608-251-5000
TELEFAX: 608-251-9166
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APPLICANT: Maxwell, I
TITLE OF INVENTION: T
TITLE OF INVENTION: I
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ADDRESSEE: Quarles &
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STRANDEDNESS:
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One South Pinckney Street
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Maxwell, Douglas P.
WENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
VENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
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                                                                                                                                                                                                                                                                                                                                               GACGACTATTTCGGAAGGGGTTCCGCTGCGCGGCCGGAAAGACCTATTAGTATCATCGTC
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GCAGAAAATACAGGTCTCAAGAACTGGACTATCAAGAATGCGATCTTCATCACCCTCACA 1020
                                                                                                                                          CAGAAAGATTGGCAATCAAATTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATC 900
                                                                                                                                                                                                              ATTGATGACATCGCACCGCATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTGGGGGCC
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                                     CCATCAATCGTGTTGCAATCCAGGTGAGGGTTCCAGTTATAAAGACTTCCTCGACAAA 1428
                                                               CCAGCAATCGTGCTTTGCAATCCTGGTGAGGGTGCCAGCTATAAAGAGTTTCTTAGACAAA 960
                                                                                                        CAAAAGGACTGGCAATCTAACTGTAAATATGGAAAGCCGGTTCAAATTAAAGGAGGAATA
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US-08-838-151A-45
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NAME: Mueller, Lisa V

REGISTRATION NUMBER: 38,978

REFERENCE/DOCKET NUMBER: SVS38

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460

TELEPAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 1183 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Circular
TOPOLOGY: Circular
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Patent No. 6
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Best Local Similarity
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APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
HYPOTHETICAL:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 1...
                                                                                                                                                                                                                                                                                                           ORGANISM: Bean Golden Mosaic Geminivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
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CLASSIFICATION: 800
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STREET: Two Prudential Plaza, Suite 4700
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                                                                                                 ATGCCCCCACCAAGAAATTTAGAGTTCAGTCAAAGAACTATTTCCTAACTTATCCCCAG
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                            TGCTCTCTATCTAAAGAAGAAGCACTTTCCCCAATTACAAAACCTAAATACCCCAGTCAAC 120
                                                                             ATGCCACCACCACAAGATTTAGAGTTCAGTCGAAAAACTATTTCCTCACTTATCCTCGT
TGCCCTATACCGAAAGAAGAAGTTCTTTCGCAACTTCAGAAGATTCATACAGCCACGAAT 120
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77.8%;
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                                                                                                                                                    Score 694.6; DB 3;
Pred. No. 4.3e-218;
0; Mismatches 239;
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RESULT 13
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 Sequence 6, Application US/09065999
Patent No. 6118048
GENERAL INFORMATION:
APPLICANT: Maxwell, Douglas P.
APPLICANT: Maxwell, Douglas P.
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Stephen F., Douglas P.
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SEQUENCE CHARACTERISTICS:

LENGTH: 1651 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic

US-09-065-999-6
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENTIN PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PLATA:
SOFTWARE: PATENTIN PATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,999
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NAME: Seay, Nicholas J.

REGISTRATION UNMBER: 27,386

REFERENCE/DOCKET NUMBER: 9602

TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-500

TELEPHONE: 608-251-506
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: TR.
TITLE OF INVENTION: DN.
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
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STATE: WI
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                   CAAAATCATAACATCCGCTCTAACCTAGAACGAATATTCGCAAAGGCTCCGGAACCGTGG
                                                                  GGTTCGGTTCAATCTGCCCTTAGCGGTTCTAAGGGAAGAACAACCAAAAGATTTTGTATTA
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                                               GATTCAATTGAATCTGCCTTGACAATATTGAAGGAAGAACAACCGAAAGATTACGTCCTT
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Pred. No. 5.3e-218;
0; Mismatches 239;
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RESULT 14
US-08-838-151A-48
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APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
COMPUTER: PC COMPATION SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      STREET: Two Pr
                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                              STATE: Illinois
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Dressler, Rockey, Milnamow & Katz STREET: Two Prudential Plaza, Suite 4700
                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          601 GATAATTATTTCGGGACGGGTGACGCTGCGCCGCCGGATAGACCTGTAAGTATCATCGTC
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
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ANTI-SENSE:
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LOCATION:
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STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
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                                         AGAGGTGATTCACGAACCGGAAAGACAATGTGGGCTCGTGCATTAGGACCACATAATTAT
                                                               GATAATTATTTCGGGACGGGTGACGCTGCGCCGCCGGATAGACCTGTAAGTATCATCGTC
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CTCAGTGGACACCTAGACTTCAATGGTCGAGTCTTCTCGAATGATGTGCAGTATAACGTC
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Pred. No. 5.4e-217;
0; Mismatches 228;
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                                                                                                                                                        CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MUELLER, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3I
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEPAX: 312-616-5400
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 51, Application US/08838151A Patent No. 6291743
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APPLICANT: Stout, John T

APPLICANT: Luw, Hang T

APPLICANT: Maxwell, Douglas

APPLICANT: Malquist, Paul

APPLICANT: Hanson, Steve

TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus

NUMBER OF SEQUENCES: 63
                                           TOPOLOGY: circular MOLECULE TYPE: DNA (go HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ORGANISM: Bean Gold STRAIN: Type II INDIVIDUAL ISOLATE:
                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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STREET: Two Prudential Plaza, Suite 4700
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3: Illinois
IRY: U.S.A.
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                                Bean Golden Mosaic Geminivirus
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                                                                                                                                                                                                                                CTCAGTGGACACCTAGACTTCAATGGTCGAGTCTTCTCGAATGATGTGCAGTATAACGTC
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                                             CCAGCAATCGTGCTTTGCAATCCTGGTGAGGGTGCCAGCTATAAAGAGTTCTTAGACAAA
                                                                               CAPAAGGACTGGCAATCTPACTGTPAATATGGAAAGCCGGTTCAPATTAPAGGAGGAGTA
                                                                                                             CAGAAAGATTGGCAATCAAATTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATC
                                                                                                                                                                            ATTGATGACATCGCACCGCATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTGGGGGCC
                                                                                                                                                                                                                                                                              GAAGGTGATTCACGAACCGGACACACAATGTGGGCTCGTGCATTAGGACCACATAATTAT
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                  CCATCAATCGTGTTGTGCAATCCAGGTGAGGGTTCCAGTTATAAAGACTTCCTCGACAAA
                                                                                                                                               ATTGATGACATAAGCCCCAATTATTTGAAGTTAAAGCACTGGAAAGAACTAATTGGGGCA
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Pred. No. 5.4e-217;
0; Mismatches 228;
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Oy  961 GCAGAAAATACAGGTCTCAAGAACTGGACTATCAAGAATGCGATCTTCATCACCCTCACA 1020  Db 961 GAAGAAAACCGAGCTTTACACAACTGGACTATTCATAATGCGATCTTCGTCACCCTCACA 1020  Oy 1021 GCCCCCCTCTATCAAGAGAGCACACAGGCAAGCCAA 1056  Db 1021 GCCCCCCTCTATCAAGAGACACAGGATTGCCAA 1056  Search completed: December 4, 2004, 16:17:42  Job time: 120 secs
961 GCAGAAATACAGGTCTCAAGAACTGGACT
GCAGAAAATACAGGTCTCAAGAACTGGACT

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Result
No.
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Maximum DB seq length: 200000000
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
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Match
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Gapop 10.0 , Gapext 1.0
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1083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq: *
/ Cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq: *
/ Cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq: *
/ Cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq: *
/ Cgn2 6/ptodata/1/pubpna/US10 PUBCOMB.seq: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_ENE_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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    US-08-838-151A-1
US-08-838-151A-7
US-08-838-151A-7
US-08-838-151A-17
US-08-838-151A-13
US-08-838-151A-13
US-08-838-151A-43
US-08-838-151A-45
US-08-838-151A-45
US-08-838-151A-45
US-08-838-151A-45
US-08-838-151A-45
US-08-838-151A-45
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Sequence 15, Appli
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Sequence 51, Appli
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US-08-838-151A-60	US-08-838-151A-59	US-10-633-850-111	-10-633-850	US-08-838-151A-29	838-151A-2	-838-151A-	08-838-151A-1	-10-633-850-6	US-10-633-850-55	-10-633-850-5	-10-633-850-5	-10-633-	50-7	-10-633-850	-10-633-850-6	US-10-633-850-59	-10-633-850	-10-633-850-8	0	0-633-850-7	US-10-633-850-65	-10-633-	-10-633-850-9	0-9	0-633-850-8	US-10-633-850-81	0-633-850-9	US-10-633-850-91	-10-633-850	-10-633-850-5	US-10-633-850-83	US-10-633-850-79
Sequence 60, Appl	equence 59, Ap	Sequence 111, App	ce 110,	e 29,	26,	23,	19,	Sequence 69, Appl	e 55,	53,	51,	Sequence 75, Appl	73,	71,	67,	59,	57,	89,	87,	77,		61,	97,	95,	æ	e 81,	e 93,	91,	63,	50,	83,	•

## ALIGNMENTS

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US-08-838-151A-1
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FILING DATE:
CLASSIFICATION: 800
ATTORNEY, AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz
                                                                                                                                                                                                                                                                                                                                 STATE: I
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                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                      Illinois
                                                                                                                                                                                                                                                                                                                                                                                                 E: Dressler, Rockey, Milnamow & Katz
Two Prudential Plaza, Suite 4700
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUBLICATION: 44......
PUBLICATION INFORMATION:
AUTHORS: Gilbertson, RI
AUTHORS: Hidayat, SH
AUTHORS: Foromatas, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1162 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Tomato Mottle Gemini Virus INDIVIDAL ISOLATE: Florida FEATURE: NAME/KEY: CDS
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE: dwar
JOURNAL: JO
VOLUME: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAGES: 23-31
DATE: 1993
                                                                                                                               421
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GTTCCTCCATTTCAAGTCTCTTTCACTAACGTTCCTGACGAGATGCAGGAATGGGCG
                                                   CAAAATCATAACATCCGCTCTAACCTAGAACGAATATTCGCAAAGGCTCCGGAACCGTGG
                                                                                                                    GGTTCGGTTCAATCTGCCTTAGCGGTTCTAAGGGGAAGAACAACCAAAAGATTTTGTATTA
                                                                                                                                                               AGATCTGCCAGAGGAGGCCAGCCAGTCTGCTAATGATTCATATGCGAAAGCGTTAAATGCA
                                                                                                                                                                                AGATCTGCCAGAGGAGGCCAGCAGTCTGCTAATGATTCATATGCGAAAGCATTAAATGCA
                                                                                                                                                                                                                                                   AAATCATACATCGACAAGGACGGAGATACAATCGAATGGGGAGATTTTCCAAATCGACGGC
                                                                                                                                                                                                                                                                                                                     CCAACCCGGTCAGCACATTTCCATCCGAATATTCAGGGGAGCTAAATCGAGCTCCGACGTC
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Pseudorecombination between the infectious
Cloned DNA components of tomato mottle and bean
dwarf mosaic geniniviruses.
L: Jour. General Virol.
                                                                                                                                                                                                                               AAATCGTACATCGACAAGGACGGAGATACAATCGAATGGGGAGATTTCCAGATCGACGGC
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Rojas, MR
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RESULT 2
US-08-838-151A-5
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                                                                                                                                                                                                                                                                                                    APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Pl
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
FILING DATE:
CLASSIFICATION: 800
ATTORNEY AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                      STREET: Two Pruc
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                        ZIP: 60601
                                                                                                      APPLICATION NUMBER:
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Two Prudential Plaza, Suite 4700
                                                                                                                                                                                                                                        U.S.A.
                                                                                                      US/08/838,151A
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                                                                                                                                       Version
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEPAX: 312-6146-5460
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Gemini Virus
STRAIN: Florida
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LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
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CTCAGTGGACACCTAGACTTCAATGGTCGAGTCTTCTCGAATGATGTGCAGTATAACGTC
                                 GAGGGTGATTCAAGAACAGGGCACACGATGTGGGCACGTGCGTTAGGCCCCACATAACTAT
                                                    GATAATTATTTCGGGACGGGTGCAGCTGCGCGGCCAGAGAGACCTGTAAGTATCATCGTC
                                                                                                                                 GATAATTATTTCGGGACGGGTGACGCTGCGCCGCCGGATAGACCTGTAAGTATCATCGTC
                                                                                                                                                                                                 GTTCCTCCATTTCAAGTCTCTTCTTTCACTAACGTTCCTGACGAGATGCAGGAATGGGCG
                                                                                                                                                                                                                                  CAAAATCATAACATCCGCTCTAACCTAGAACGAATATTCGCAAAAGGCTCCGGAACCGTGG
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97.8%;
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Pred. No. 2.46
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2.4e-312;
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                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5400
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1169 base pairs
TYPE: nucleic acid
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
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STATE: Illinois
COUNTRY: U.S.A.
                                     TOPOLOGY:
                                                STRANDEDNESS: single
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CLASSIFICATION: 800
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Best Local Similarity 97.7
Matches 1058; Conservative
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LOCATION:
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                                                           CAGAAAGATTGGCAATCAAATTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATC
                                                                                                       ATTGATGACATCGCACCGCATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTGGGGGCC
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US-08-838-151A-17
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US-08-838-151A-17/c
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2602 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
                                                             Best Local Similarity Matches 1054; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/08838151A Publication No. US20010011379A1 GENERAL INFORMATION:
                                                                                                                              APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Maxwell, Douglas
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSER: Nocanian Plants
                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MUELLET, LISA V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SV:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: ...STREET: Chicago
CITY: Chicago
TMATE: Illinois
TH.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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Two Prudential Plaza, Suite 4700
                                                             96.1%;
ilarity 98.0%;
Conservative
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                                                             Score 1040.8; DB 8
Pred. No. 5.5e-311;
0; Mismatches 22;
                                                                                            DB 8;
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US-08-938-151A-3 iS-08-938-151A-3 i Sequence 3, Application US/08838151A i Publication No. US20010011379A1

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; JOURNAL: JOURT
; VOLUME: 74
; PAGES: 23-31
; DATE: 1993
US-08-838-151A-3
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ATTORNEY/AGENT INFORMATION:
NAME: MUELLER, LISA V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: 5V53:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 base pairs
TYPE: nucleic acid
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APPLICANT: Stout, John T
APPLICANT: Lu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Marwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Pl
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Mi
                                                                                                                                                                                                                               Query Match
Best Local Similarity 97.9
Matches 1056; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 44..1127
PUBLICATION INFORMATION:
AUTHORS: Gilbertson, RL et al.
TITLE: Pseudorecombination between the infectious
TITLE: cloned DNA components of tomato mottle and
TITLE: dwarf mosaic geminivirus.
JOURNAL: Journal of General Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Gemini Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN: Florida
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two P. CITY: Chicago
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                                                                                                    TGCTCTATCTAAAGAAGAAGAACTTTCCCAATTACAAAACCTAAATACCCCAGTCAAC
                  AAGAAATTCATCAAAATTTGCAGAGAGACCTTCATGAAAATGGGGAACCTCATCTCCATGTG 180
                                                                         TGCTCTTTGTCTAAAGAAGAAGCACTTTCCCAATTACAAAACCTAAATACCCCAGTCAAT
AAGAAATTCATCAAAATTTGCAGAGAGCTTCATGAAAATGGGGAACCTCATCTCCATGTG
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Two Prudential Plaza, Suite 4700
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RESULT 6
US-08-838-151A-13
US-08-838-151A-13
Sequence 13, Application US/08838151A
Publication No. US20010011379A1
GENERAL INFORMATION:
APPLICANT: Stout, John T
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REFERENCE/DOCKST NUMBER: SVS3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1166 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 95.5%;
Best Local Similarity 97.6%;
                                                                                                                                                                                                                                                                                                                                                                                        Matches 1061;
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NAME/KEY:
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CORRESPONDENCE ADDRESS: Rockey, Milnamow & STREET: Two Prudential Plaza, Suite 4700
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APPLICANT: Ahiquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
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ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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AAATCATACATCGACAAGGACGGAGATACAATCGAATGGGGAGATTTCCAAATCGACGGC
                                                                                  CCAACCCGGTCAGCACATTTCCATCCGAATATTCAGGGAGCTAAATCGAGCTCCGACGTC
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Sequence 15, Application US/08838151A
Publication No. US20010011379A1
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Ahlquist, Paul
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plant
TITLE OF INVENTION: Genes
UNMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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US-08-838-151A-15
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ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
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ATTORNEY/AGENT INFORMATION:
NAME: MUGALLEY, LISA V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1246 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 64.8
Best Local Similarity 98.2
Matches 710; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Tomato Mottle (
STAIN: Florida
PUBLICATION INFORMATION:
AUTHORS: Gilbertson, RL
AUTHORS: Hidayat, SH
AUTHORS: Paplomatas, EJ
AUTHORS: Paplomatas, EJ
AUTHORS: Rojas, MR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS: Hou, YM
AUTHORS: Maxwell, DP
TITLE: Pseudorecombination between the infectious
TITLE: cloned DNA components of tomato mottle and
TITLE: dwarf mosaic geminiviruses.
JOURNAL: Journal of General Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAGES: 23-31
DATE: 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL: JO
VOLUME: 74
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STRANDEDNESS: single
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GAGGGTGATTCAAGAACAGGGAAGACGATGTGGGCACGTGCGTTAGGCCCACATAACTAT
                                                                      GATAATTATTTCGGGACGGGTGCAGCTGCGCGGCCAGAGACACCTGTAAGTATCATCGTC
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RESULT 8
US-08-838-151A-43
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"ublication NU."

GENERAL INFORMATION:

GENERAL INFORMATION:

Hang T
                                                                                                                                                                                                                                                                                                                            ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Alquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Pl
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
                                                                                                                             TELEFAX: 312-616-5460 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1183 base pairs
                                                                                                                                                           REFERENCE/DOCKET NUMBER: SV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSE: Dressler, Rockey, Milnamow & Katz
ADDRESSE: Two Prudential Plaza, Suite 4700
   HYPOTHETICAL:
                    MOLECULE TYPE:
                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 800
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                                                                                        LENGTH:
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                    (genomic)
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Matches
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PUBLICATION INFORMATION:
AUTHORS: Faria, JC
AUTHORS: Gilbertson, RI
AUTHORS: Hanson, SF
AUTHORS: Morales, FJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Geminivirus
STRAIN: Type II Isolates
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VOLUME: 84
ISSUE: 3
PAGES: 321-
DATE: 1994
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TITLE: G
TITLE: P
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS: Morales, FJ
AUTHORS: Ahlquist, P
AUTHORS: Loniello, AO
AUTHORS: Maxwell, D
TITLE: Bean Golden Mosaic Geminivirus Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 839; Conserv
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                                                                          GTTCCTCCATTTCAAGTCTCTTTCTTTCACTAACGTTCCTGACGAGATGCAGGAATGGGCG
                                                                                                                                                  CAAAATCATAACATCCGCTCTAACCTAGAACGAATATTCGCAAAGGCTCCGGAACCGTGG
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                                                        GTTCCTCCATTTCCGTTGTCATCATTCATCAATGTTCCGGTTGTTATGCAAGAATGGGTT
                                                                                                                           CAACATCACAACATCCGTTCTAATCTCGAACGGATCTTCGTCAAAGTGCCGGAACCATGG
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Hanson, SF
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Pred. No. 2e-204;
0; Mismatches 23
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RESULT 9
US-08-838-151A-45
INFORMATION FOR SEQ ID NO: 45
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1183 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45, Application US/08838151A Publication No. US20010011379A1 GENERAL INFORMATION:
                                                                                                                    FILING DATE:
CLASSIFICATION: 800
ATTORNEY AGENT INFORMATION:
NAME: mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3
TBLECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
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                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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Two Prudential Plaza, Suite 4700
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Pred. No. 6.2e-204;
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Query Match 63.8%; Score 691.2; DB 8; Length 1062; Best Local Similarity 78.4%; Pred. No. 6.6e-203; Matches 828; Conservative 0; Mismatches 228; Indels 0; Gaps 0;	œ	; INUIVIUAL ISOLATE: GUATEMAIA ; FEATURE: · NAME/KEV. CDG	URCE: Bean Golde Type II	; HYPOTHETICAL: NO ; ANTI-SENSE: NO	rcula	LENGTH: 1062 base pairs TYPE: nucleic acid	; INFORMATION FOR SEQ ID NO: 48: ; SEQUENCE CHARACTERISTICS:	INFORMATIO	NAME: Mueller, Lisa V REGISTRATION NUMBER: 38,978 REFERENCE/DOCKET NUMBER: SVS.1801P0260	CLASSIFICATION: 800  ATTORNEY/AGENT INFORMATION:	338,151	Ø	; COMPUTER: TEM PC COMPATIBLE ; COMPUTER: TEM PC COMPATIBLE	; STATE: Illinois ; COUNTRY: U.S.A. ; ZIP: 66601	ADDRESSEE: Dressler, Rockey, Milnamow & Katz; STREET: Two Prudential Plaza, Suite 4700; CITY: Chicago	; TITLE OF INVENTION: GENES ; NUMBER OF SEQUENCES: 63 ; CORRESPONDENCE ADDRESS:	Hanson, S	; APPLICANT: Stout, John T ; APPLICANT: Luu, Hang T ; APPLICANT: Maxwell, Douglas . APPLICANT: Ablamist Davi	Application:	RESULT 10 US-08-838-151A-48	Db 1021 GCCCCCCTCTATCAAAGCACAACACAGGATTGCCAAACGTAGAGCCATTCGTCGACG 1077	QY 1021 GCCCCCCTTATCAAGAGAGACACACAGGCAAGCCAAGAAAACGGGCAATCAGAAGGCG 1077	Qy 961 GCAGAAAATACAGGTCTCAAGAACTGGACTATCAAGAATGCGATCTTCATCACCCTCACA 1020	Db 901 CCATCAATCGTGTTGTGCAATCCAGGTGAGGGTTCCAGTTATAAAGACTTCCTCGACAAA 960	841 CAAAAGGACTGGCAATCTAACTGTAAATATGGAAAGCCGGTTCAAATTAAAGGAGGAGTATAA
D 5	рь	8	ОУ	ДЬ	S	ДĎ	Q 5	ş 8	Db	\$ {	ਤੋਂ <i>\</i>	Db	γ	Оу	οb	Q E	P Q	dg Vy	מם ג	Q 5	g Q	дb	Qy Db	Q V	D, Qy
1021 GCCCCCTCTATLANAGAGCACACACAGATTGCCAA 1056 1021 GCCCCCTCTATCAAAGCACACAGGATTGCCAA 1056		961 GCAGAAAATACAGGTCTCAAGAACTGGACTATCAAGAATGCGATCTTCATCACCCCTCACA 1020	901 CCAGCAATCGTGCTATACAATCCTGGTGAGGGTGCCAGCTATAAAGAGTTCTTAGACAAA 960		841 CAGAAAGATTGGCAACCAAATTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATC 900			721 CTCAGTGGACACCTAGACTTCAATGGTCGAGTCTTCTCGAATGATGTGCAGTATAACGTC 780	AGAGGTGATTCACGAACCGGAAAGACAATGTGGGCTCGTGCATTAGGACCACATAATTAT	GAGGGTGATTCAAGAACAGGGAAGACGATGTGGGCGCGTGCGT	601 GATRATTATTTCGGGACGGGTGACGCTGCGCCGCGGGATAGACCTGTAAGTATCATCGTC 660		541 GTTCCTCCATTTCAAGTCTCTTTTCACTAACGTTCCTGACGAGATGCAGGAATGGGCG 600	481 CAAAATCATAACATCCGCTCTAACCTAGAACGAATATTCGCAAAGGCTCCGGAACCGTGG 540	GATTCAATTGAATCTGCCTTGACAATATTGAAGGAAGAACAACCGAAAGATTACGTCCTT	361 AGATICTGCANGAGGANGTICAGCAGTICTGCCAANCGACTCATATGCAAAAGACTTTTGTATTA 480 421 GGTTCGGTTCAATCTGCCTTAGCGGTTCTAAGGGAAGAACAACCAAAAAGATTTTGTATTA 480	AGATCTGCCAGAGGAGGCCAGCAGTCTGCTAATGATTCATATGCGAAAGCATTAAATGCA	301 AARTCATKCATCGACAAGGACGAGATACAATCGAATGGGGAGATTTCCAAATCGACGGC 360	TCAACCAGGTCAGCACCTTTCCATCCGAACATTCAGGGAGCTAAATCAAGTTCAGACGTC		181 CTTGTTCAGTTCGAAGGTAAGTACCAATGCACGAATAACAGATTCTTCGACCTGGTCTCC 240	121 AAAAAATTCATCAAAGTCTGTGAGGAACGTCACGAGAATGGTGAACCTCATCTTCATGCG 180	61 TGCCCTATACCGAAAGAAGAAGTTCTTTCGCAACTTCAGAAGATTCATACAGCCACGAAT 120 121 AAGAATTCATCAAAATTTGCAGAGAGAGCTTCATGAAAATGGGGAACCTCATCTCCATGTG 180	TGCTCTCTATCTAAAGAAGAAGCACTTTCCCAATTACAAAACCTAAATACCCCAGTCAAC 1	1 ATGCCCCCACCAAAGAAATTTAGAGTTCAGTCAAAGAACTATTTCCTAACTTATCCCCAG 60 

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                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/838
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEPHONE: 312-616-5460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Alquist, Paul
APPLICANT: Alquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genee
NUMBER OF SEQUENCES: 63
CORRESPONDENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DN
                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Bean Golden Mosaic Geminivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
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: Illinois
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CTTGTTCAGTTCGAAGGTAAGTACCAATGCACGAATAACAGATTCTTCGACCTGGTCTCC
                                                                                          AAGAAATTCATCAAAATTTGCAGAGAGCTTCATGAAAAATGGGGAACCTCATCTCCATGTG
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Two Prudential Plaza, Suite 4700
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                                                                                                                                                                                                                                                                             Score 691.2; DB 8;
Pred. No. 6.6e-203;
0; Mismatches 228;
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                                                                                                                                                               Sequence 54, Application US/08838151A Publication No. US20010011379A1 GENERAL INFORMATION:
                 APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
     CORRESPONDENCE ADDRESS:
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                                                         Transgenic
                                                           Plants
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840 840 780 780 720 720 660 660

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Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Geminivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION UMBER: 38,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 312-616-5400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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STREET: TV
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Local Similarity 78.3%;
nes 827; Conservative
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION: 1...
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STRANDEDNESS: single
TOPOLOGY: circular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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  GGTTCGGTTCAATCTGCCTTAGCGGTTCTAAGGGAAGAACAACCAAAAGATTTTGTATTA 480
                                                                                                                        AAGGCATACATCGACAAAGATGGAGTCACAATCGAATGGGGACAATTCCAAGTCGACGGC
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Pred. No. 2.1e-202;
0; Mismatches 229;
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                                                                                                                                                                          TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
FILE REFERENCE: 5051.4581P
CURRENT APPLICATION NUMBER: US/10/633,850
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 09/289,346
PRIOR APPLICATION NUMBER: US 09/289,346
PRIOR APPLICATION NUMBER: US 60/125,004
PRIOR APPLICATION NUMBER: US 60/125,004
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 112
SOPTWARE: Patentin version 3.2
SEQ ID NO 79
LENGTH: 1056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 79, Application US/10633850 Publication No. US20040205843A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hanley-Bowdoin, Linda
APPLICANT: Orozco, Beverly M.
APPLICANT: Gruissem, Wilhelm
                                                    NAME/KEY: CDS
LOCATION: (1)..(1056)
OTHER INFORMATION: TGMV
                                                                                                                                                                TYPE: DNA
                                                                                                                        FEATURE:
                                                                                                                                         ORGANISM: Tomato
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56.1%;
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CCCTCTATCAAGAGAGAGACACAGGGCAAGC 1053
                                                          AAAACACTCCACTAAAGAACTGGACTTTCCATAATGCGAAATTCGTCTTCCTCAACTCCC
                                                                                                                                                          CAATCGTGCTTTGCAATCCTGGTGAGGGTGCCAGCTATAAAGAGTTCTTAGACAAAGCAG
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CURRENT APPLICATION NUMBER: US/10/633,850
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 09/289,346
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 60/125,004
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin version 3.2
SEQ ID NO 83
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Publication No.
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APPLICANT: Orozco, Beverly M.
APPLICANT: Gruissem, Wilhelm
TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
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LOCATION: (1)..(105
OTHER INFORMATION:
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ORGANISM: Tomato
FEATURE:
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Pred. No. 6e-177;
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Matches
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                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.2 SEQ ID NO 50
                                                                                                                                                     Query Match
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APPLICANT: Orozco, Beverly M.
APPLICANT: Gruissem, Wilhelm
TITLE OF INVENTION: GEMINIVIRUS RESISTANT
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/289,346
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 60/125,004
PRIOR FILING DATE: 1999-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 5051.458IP
CURRENT APPLICATION NUMBER: US/10/633,850
CURRENT FILING DATE: 2003-08-04
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 112
                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (1)..(1056)
OTHER INFORMATION: TGMV AL1 coding
                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Tomato
FEATURE:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

ORIGIN	FEATURES Bource	KEYWORDS SOURCE SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED COMMENT	RESULT 1 BZ394806/c LOCUS DEFINITION ACCESSION VERSION
/organism="Entamoeba invadens" /mol_type="genomic DNA" /mol_type="genomic DNA" /mol_type="genomic DNA" /strain="IP-1" /db_xref="taxon:33085" /clone="giNB009" /clone="bl="EII0_12_KB" /clone="vector: pHOS2; Site_1: BstXI; Total genomic DNA was isolated from early log phase trophozoites of E. invadens IP-1 using a Qiagen plant DNA extraction kit. A shotgun medium-size plasmid library (average insert size of 10 - 12 kb) was generated by random mechanical shearing of E. invadens genomic DNA, repairing the ends of DNA fragments with T4 Polymerase, adding BstXI adaptors and ligating into the BstXI site of a pUC-derived vector pHOS2."	Contact: Brendan Loftus Department of Eukaryotic Genomics TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA 9712 Medical Center Drive, Rockville, MD 20850, USA 7el: 301-838-0208 Email: enta@tigr.org DNA was provided by Daniel Eichinger Seg primer: TF Class: sheared ends. Location/Qualifiers 1636 //organism="Entamoeba invadens"	GSS.  GSS.  Entamoeba invadens  Entamoeba invadens  Entamoeba invadens  Eukaryota; Entamoebidae; Entamoeba.  1 (bases 1 to 636)  Wang, Z., Samuelson, J., Clark, C.G., Eichinger, D., Paul, J., van  Dellen, K., Hall, N., Anderson, I. and Loftus, B.  Gene discovery in the Entamoeba invadens genome  Mol. Biochem. Parasitol. 129 (1), 23-31 (2003)  22684048  12798503  Other_GSSs: EINBO09TR	BZ394806 636 bp DNA linear GSS 30-APR-2003 EINBOO9TF EI 10 12 KB Entamoeba invadens genomic clone EINBOO9, genomic survey sequence. BZ394806 BZ394806 1 GI:30241347

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                                                                                                                                                                                                                                                                                                                                                                                       Fizames,C., Pischer, C., Durcher, J., Saurin,W., Bernot,A. and Weissenbach,J.

Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)
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                                                                                                                                                    Submitted (12-APR-2000) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a larg scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tetraodon
071D12 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Estimate of human gene number provided by genome-wide analysis using Tetracdon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL268481.1 GI:7990330
GSS; genome survey sequence.
Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                      Genoscope
Direct Submission
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              /organism="Tetraodon nigroviridis"
/mol type="genomic DNA"
/db_xref="taxon:99883"
/clone="071D12"
/clone="071D12"
/clone_lib="G"
/note="Genoscope sequence ID : COB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nigroviridis genome surve
library G from Tetraodon
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CO088898.1
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                                                                                                                                                                                                                                                                                                                                                                                                              Email: http://genome.arizona.e
Plate: 08 row: B column: 20.
Location/Qualifiers
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Udall, J.A., Rapp, R.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arizona Genomics Institute
The University of Arizona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Rod A. Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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 TTAATACTGTACAATCCTGTAGTCGCCTAAGACCTATTAGGGAAAATAGAGCAAGCCAAG
                             ATCGTGCTTTGCAATCCTGGTGAGGGTGCCAGCTATAAAGAGTTCTTAGACAAAGCAGAA
                                                              GAGTGGGCAACAAGGGATATGGACAGTATAACCCTTCAAATCAAATAGGCCATCAACGAG
                                                                                           GATTGGCAATCAAATTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATCCCAGCA
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m;H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
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                                                                                                                                                                                                   /clone_lib="GR_Ba" | Colone | Site_1: NotI; Site_2: /note="Vector: pCMV.SPORT-6.1; Site_1: NotI; Site_2: EcoRV; Library made by Invitrogen with RNA supplied by Wendle lab. Directional cloned into NotI-EV. Colonies plated/picked by AGI. More glycerol clones held in -80
                                                                                                                                                                                                                                                                                                                                                 organism="Gossypium raimondii"
/mol_type="mRNA"
/db_xref="taxon:29730"
                                                                                                                                                                                                                                                                                  tissue_type="whole seedlings"
/dev_stage="first true leaves"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                  clone="GR_Ea08B20"
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Pred. No. 0.
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raimondii cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3143 row: B column: 1
Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                      98;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 864)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Mahairas,G.S., Wallace,J.C., Smith,K., Zhao,S., Adams,M.D. au
Wolfer,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. au
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ891340
864 bp DNA linear GSS 10-NOV-1999
HS_3143_A1_C01_T7C CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3143 Col=1 Row=E, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ891340.1 GI:6347530
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       TCTGCTAATGATT 397
                                                   TTTATTAACCTGTCTGAAAGATGACTAGTTAGCAGCAGGTTTTCCAGTAGAGTGGGATAA 411
                                                                                                                                       TTGÁCTGTGAÁCGGGGTÁGÁTTTÁCATCCAÁTGTTÁTATÁTATÁTCTCCTTÁTTGÁGGGC
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                                                                                           GATACAATCGAATGGGAAGATTTCCAAAATCGACGGCAGATCTGCCAGAGGAGGCCAGCAG 384
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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CNS011PO/c
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- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton project grant are pavan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 TCTATCTAAAGAAGAAGCACTTTCCCCAATTACAAAACCTAAATACCCCCAGTCAACAAGAA
BW370082 BW370082 Yutaka Satou unpublished cDNA library, mature adult whole animal Ciona intestinalis cDNA clone cima849d15 5', mRNA sequence.
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AL100566.1 GI:5612177
GSS.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CCCACCAAAGAATTTAGAGTTCAGTCAAAGAACTATTTCCTAACTTATCCCCAGTGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope.
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Similarity 39.0%;
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN06K06"
/clone lib="DrosBAC"
/plasmId="pBeloBAC11"
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Pred. No. 1.4;
9; Mismatches 121;
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AV957294/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        681 GAAGACGATGTGGGCGCGTGCGTTAGGCCCACATAACTATCTCAGTGGACACCTAGACTT
                                                            Contact: Nori Satch
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                       Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T. Expressed genes in Ciona intestinalis Unpublished (2000)
                                                                                                                                                                                                                                                     Ciona intestinalis
Ciona intestinalis
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Sakyo-ku, Kyoto, Kyoto 606-8502,
Tel: 81-75-753-4095
Fax: 81-75-705-1113
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
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                               Email: satoh@ascidian.zool.kyoto-u.ac.jp.
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Location/Qualifiers
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Department of Zoology
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Phlebobranchia; Cionidae; Ciona.
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   /organism="Ciona intestinalis"
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/dev stage="mature adult"
/clone lib="Yutaka Satou unpublished cDNA library, mature
adult whole animal"
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/mol_type="mRNA"
/db_xref="taxon:7719"
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                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr )

- Web : www.genoscope.cns.fr )

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 697)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fly), genomic survey sequence.
AL109511
AL109511.1 GI:5629815
GSS.
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AAAWWWTTAWAAWAATAAAAAAAAATTWAAAAAAAACTATWTYTYWTTATAWA
                                       AAAGAAATTTAGAGTTCAGTCAAAGAACTATTTCCTAACTTATCCCCAGTGCTCTATC
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/clone="cleg14903"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library,
                                                                                                                                                                                      /clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : T7"
                                                                                                                                                                                                                                                   /organism="prosophila melanogaster"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db xref="taxon:7227"
/clone="BACN14C07"
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/db_xref="taxon:
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39.1%;
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                                                                                                    Score 40.4; DI Pred. No. 1.7;
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Pred. No. 1.7;
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72 TAAAGAAGAAGCACTTTCCCAATTACAAAACCTAAATACCCCAGTCAACAAGAAATTCAT 131

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RESULT 10
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                                                                                                                                         858 AAATTGCAAGTACGGTAAGCCAGTTCAAATTAAAGGCGGAATCCCAGCAATCGTG 912
                                                                                                                                                                            120 TCAGTTCCTATAGAAAACGAACTGTAAA-CCTATCTGCAGACCATGCAAGAGGCACAATA
                                                                                                                                                                                                                 798 GCATTATCTAAAGCTAAAGCACTGGAAAGAATTGCTGGGGGCCCAGAAAGATTGGCAATC
                                                                                                                                                                                                                                                                                   738 CTTCAATGGTCGAGTCTTCTCGAATGATGTGCAGTATAACGTCATTGATGACATCGCACC
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     BX262586
BX262586
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Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusumoki-cho, Chuo-ku, Kobe, Hyogo 650-0017,
Tel: 81-78-382-5360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H., Takeda,J., Ohara,O. and Seino,S.
Construction of a multi-functional cDNA library specific for pancreatic islets and its application to microarray Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP764040 BP764040 mouse (C57BL/6) pancreatic islet library with recombination-based method Mus musculus cDNA clone mic30074 3',
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Nishimura, M., Yokoi
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Similarity 55.4%;
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Location/Qualifiers
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                                                                                                          AAACTTGAAGTGAAAAAAAAAAAAAAAAAAAAAGCGGCCGCCCAGCTTTCTTG
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739 bp mRNA linear EST 24-MAY-2004 AGENAE Gallus gallus multi-tissues normalized and
                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="pancratic islet"
/dev_stage="adult"
/clone_lib="mouse (C57BL/6) pancreatic islet library with
recombination-based method"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="mic30074"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
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Pred. No. 2.6;
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   RESULT 11
CNSOA7F8
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BX262586
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Gallus gallus
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                                                                                                        TCTTTCACTAACGTTCCTGACGA 584
                                                                       GCTTCCACAATGCTGCAGTGGA 433
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/mol_type="mRNA"
/db_xref="taxon:9031"
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502 AACCTAGAACGAATATTCGCAAAAGGCTCCGGAACCGTGGGTTCCTCCATTTCAAGTCTCT 561
                                                                                                                                       291 AGTCTTCAAAATGAGGAAAAACCAAAAGGACTAGATCTTCTAGGAACATTTACAACTTCT 350
                                                                                                                                                                                                   442 GCGGTTCTAAGGGAAGAACAACCAAAAGATTTTGTATTACAAAATCATAACATCCGCTCT
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INRA, UMR INRA-ENSAR Genetique Animale
65, rue de Saint-Brieuc, RENNES cedex,
Tel: +33 (0) 2.23.48.54.63
Fax: +33 (0) 2.23.48.54.70
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Construction and primary characterization
multi-tissue cDNA libraries
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: Madeleine.Douaire@roazhon.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 739)
Herault, F., Le Meuth-Metzinger, V., Desert, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
GACCCTGGTCCCTTAATTCCAGACTCCCTGGCACGTGATGTTTCTCCACTCCCTTTTACT
                                                                                                                                                                                                                                                                          CAGTGTGGTCCTATTTCTGATTTAAGCAAACTGCTTGAAGAACTGAGAAGCCTGCATCA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      marrow, caecum, duodenum, embryos, fabricius gland, granulosa, hypothalamus, ileon, jejunum, oviduct, pancreas, skin, spleen, thymus, utero-vaginal gland, pituitary gland, hematopoietic progenitor cells, small follicle. Clone distribution: AGENAE Resource centre. Francois PIUMI, Francois.Piumi.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="AGENAE Gallus gallus multi-tissues normalized and once-subtracted cDNA library (gcal)" (note-"Vector: pT7T3D-pac; tissues: adipose tissue, brain, kidney, liver, multi-tissues, muscle, ovary, testis, bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="gcal0008c.h.19"
/tissue_type="multi-tissues"
/dev_stage="from_embryos to adults"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                      Score 39.8; DB 5; Length 739; Pred. No. 2.7; O; Mismatches 102; Indels
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250 TCAGCACATTTCCATCCGAATATTCAGGGAGCTAAATCGAGCTCCGACGTCAAATCATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNSOA7F8 2433 bp mRNA linear HTC Arabidopsis thaliana Full-length cDNA Complete sequence GSUTLS16ZF06 of Adult vegetative tissue of strain col-0 Arabidopsis thaliana (thale cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G. Genoscope members carried out sequencing and annotation: Castell V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 2433)
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis
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                                                                                                                                                                AAGGGTAAGGATAGAGAAAGAGTTGGAATGGGAAATAACAATAATGATGGGAAGGTTAAC
                                                                                                                                                                                                        ATCGACAAGGACGGAGATACAATCGAATGGGGAGATTTCCAAATCGACGGCAGATCTGCC
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                                                                               AGAAGAAGGGAGCAAATGGCAGATGATTCTGACTATTCAAGAAATTCCGGCGATAAGTCT
                                                                                                                         AGAGGAGGCCAGCAGTCTGCTAATGATTCATATGCGAAAGCATTAAAATGCAGGTTCGGTT
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/gene="At3g15220"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3702"
/clone="GSLTLS16ZF06"
/tissue_type="Adult vegetative tissue"
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strain="Col-0"
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Pred. No. 4.1;
0; Mismatches 114; Indels
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PUHMZ34TB ZM 0.6_1.0_KB Zm
genomic survey sequence.
CC375636
CC375636.1 GI:30849253
GSS.
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TIGR
9712 Medical Center Drive,
Tel: 301-838-5843
                                                                                                                                                                 1 (bases 1 to 762)
1 (bases 1 to 762)
whitelaw,C.A., Quackenbush,J., Vai
                                                                                         Unpublished (2003)
Other_GSSs: PUHMZ34TD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 738)
Humphray, S.J., Huckle, E. and Durham, J.L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Danio rerio
BX200121
                                                                   Contact: Cathy Whitelaw
                                                                                                                               Maize Genomics Consortium
                                                                                                                                                    Bennetzen, J
                                                                                                                                                                                                                                  clade; Panicoideae; Andropogoneae;
                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; E
Spermatophyta; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                              Zea mays
                                                                                                                                                                                                                                                                                                                   Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/Projects/D_rerio/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keygene. Further details:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was generated from the SP6 end of BAC 210B11. 210B11 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Campus, Hinxton, Cambridgeshire, (
humquery@sanger.ac.uk Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (27-JAN-2003) The Sanger Institute, Wellcome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Danio rerio
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
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/tissue_type="Testis"
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genomic clone ZMMBTa488E20,
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a; Poales; Poaceae; PACCAD
                             20850,
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                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 933)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                              Unpublished (2003)
Other GSSs: PUGCL17TB
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence BZ826521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BZ826521 933 pp DNA ILLIGAL SUCLITOR ZMMBTa336D10,
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Class: sheared ends.
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Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                 Maize Genomics Consortium
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                                                                                                                                                                                                                          Email: whitelaw@tigr.org
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CG168857
CG168857.1 GI:34059658
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Cathy Whitelaw
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                                                         TATTCATAGAGACTCAGGATCATCGGGTTCATCCAGTAAAAGTACATCCTTAAATCCAAG
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1499 77.3 356 3 AAB18687	Result 1.22.2.1 1.33.4 4.4 1.0 1.0 1.0 1.0 1.1 1.1 1.1 1.2	Score 1908 1902 1892 1875 1575 1575 1576 1567 1566 1566 1566 15
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AAW82413	AAW82414	AAB18682	AAB18683	AAB18689	AAB18678	AAB18680	AAB18684	AAB18692	AAB18690	AAB18679	AAB18685	AAB18681	AAB18686	AAB18688	AAB18691	AAB18677	AAY92706	ADM48184	CO LECTUR
Aaw82413 TGMV	Aaw82414	Aab18682	Aab18683	Aab18689	Aab18678	Aab18680	Aab18684	Aab18692	Aab18690	Aab18679	Aab18685	Aab18681	Aab18686	Aab18688	Aab18691	Aab18677	Aay92706	Adm48184	nayaaroo
TGMV AL1	BGMV AL1	Mutant pe	Mutant	Mutant pe	Mutant	Mutant	. Mutant pe	Mutant pe	Mutant pe	. Mutant pe	Peptide f		Polypepti						

## ALIGNMENTS

RESULT 1
AAW34336
ID AAW3
AC AAM3
AC AAW3
AC AAM3
AC AAW3
AC AAM3
AC AAW3
AC AAM3
AC AAW3
AC AAM3
AC AAW3
AC A 17-OCT-2003 27-APR-1998 16-APR-1996; 15-APR-1997; 23-OCT-1997. WO9739110-A1 Tomato mottle virus; isolate Florida. disease resistance. Geminivirus; ToMoV; AC1 gene; transdominant mutation; transgenic plant; Tomato mottle virus AC1 protein. AAW34336; AAW34336 standard; protein; 361 (revised) (first en 96US-0015517P. 97WO-US006300 entry) ጅ

Stout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;

(SEMI-) SEMINIS VEGETABLE SEEDS INC. (WISC ) WISCONSIN ALUMNI RES FOUND.

WPI; 1997-526447/48. N-PSDB; AAT93294.

Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mottle virus, tomato yellow leaf curl virus or bean golden mosaic

Example 3.3; Page 57-58; 132pp; English.

This protein comprises the wild-type AC1 protein of tomato mottle virus (ToMoV), a geminivirus that has a bipartite genome. The AC1 gene (see AAT93294) must be expressed for efficient replication of the two genomic components, DNA-A and DNA-B. The AC1 protein has a DNA binding site specific to the DNA-A common region, a DNA nicking activity, and an NTP binding activity. The invention involves production of transgenic plants containing DNA comprising AC1 or C1 wild-type or mutant sequences that negatively interfere in trans with geminiviral replication during infection. Such transgenic plants are resistant to viral infection. The

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ARESULT 2
AAW34325
ID AAW3
XX AAW3
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Best Local Similarity
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                              N-PSDB; AAT93283
                                                       WPI; 1997-526447/48
                                                                                                           Stout JT,
                                                                                                                                                                                                                                           16-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tomato mottle virus; isolate Florida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic plant; disease resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Geminivirus; ToMoV-ACIdlm1; ACI gene; transdominant mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tomato mottle virus AC1 mutant ToMV-AC1dlm1.
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                                                                                                                                                             (SEMI-) SEMINIS VEGETABLE SEEDS INC. (WISC.) WISCONSIN ALUMNI RES FOUND.
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98.3%;
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Pred. No. 4.5e-169;
                                                                                                         Ahlquist PG;
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Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mottle virus, tomato yellow leaf curl virus or bean golden mosaic
                                                                                                                                                        Example 3.5; Page 64-65; 132pp; English.
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This protein comprises a transdominant lethal mutant, designated ToMoV-ACIDIMI, of tomato mottle virus (TOMOV) ACI protein (see AAM34336). It is encoded by a mutant ACI gene (see AAM33333) of tomato mottle virus virus (TOMOV), and carries a mutation in an NTP-binding domain. The ACI gene (see also AAT93294) must be expressed for efficient replication of the two genomic components, DNA-A and DNA-B, of the bipartite TOMOV genome. The invention involves production of transgenic plants containing DNA comprising geminivirus ACI or Cl wild-type or mutant sequences that negatively interfere in trans with geminiviral replication during the infection. Such transgenic plants are resistant to viral infection. The ACI genes are especially from TOMOV, tomato yellow leaf curl virus or bean golden mosaic geminivirus (see AAT93282-93) and encode polypeptides (see AAW34324-35) that have mutations in the highly conserved DNA-nicking and/or NTP-binding domains

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Sequence 361 AA
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uery Match	uery Match 98.1%; Score 1902; DB 2; Length 361;	
latches 3	vative 3; Mismatches 4; Indels 0; Gaps	0;
	1 MPPPKKFRVQSKNYFLTYPQCSLSKEEALSQLQNLNTPVNKKFIKICRELHENGEPHLHV 60	0
	1 MPPPKKFRVQSKNYFLTYPQCSLSKEEALSQLQNLNTPVNKKFIKICRELHENGEPHLHV 60	9
61	1 LVQFEGKYQCTNNRFFDLVSFTRSAHFHPNIQGAKSSSDVKSYIDKDGDTIEWGDFQIDG 120	20
61	1 LVQFEGKYQCTNNRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDTIEWGDFQIDG 120	20
. 121	1 RSARGGQOSANDSYAKALNAGSVQSALAVLREEQPKDFVLQNHNIRSNLERIFAKAPEPW 180	80
121	1 RSARGGQQSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHNIRSNLERIFAKAPEPW 180	80
181	1 VPPFQVSSFTNVPDEMQEWADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMWARALGPHNY 240	0
181	1 VPPFQVSSFTNVPDEMQEWADNYFGTGAAARPERPVSIIVEGDSRTGHTMWARALGPHNY 240	40
241	1 LSGHLDFNGRVFSNDVQYNVIDDIAPHYLKLKHWKELLGAQKDWQSNCKYGKPVQIKGGI 300	00
241	1 LSGHLDFNGRVFSNDVQYNVIDDIAPHYLKLKHWKELLGAQKDWQSNCKYGKPVQIKGGI 300	00
301	1 PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTQASQETGNQKAQ 360	60
301	1 PAIVLCNPGEGASYKEFLDKAENTGLKNWTVKNAIFITLTAPLYQDSTQASQETGNQKAQ 360	60
361	1 G 361	
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AAW34326 standard; protein; 361

AAW34326;

27-APR-1998 (first entry)

Tomato mottle virus AC1 mutant ToMV-AC1dlm23.

transgenic Geminivirus; ToMoV-AC1dlm23; AC1 gene; plant; disease resistance. transdominant mutation;

ARM3433 ARM34333 XX ARM3 AC ARM3 AC ARM3 AC Toma XX Toma XX Toma XX Toma XX Gemi XX Toma XX Toma Tomato mottle virus; isolate Florida Synthetic.

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Best Local Similarity
Matches 353; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This protein comprises a transdominant lethal mutant, designated ToMoV-ACIdna3, of tomato mottle virus (TOMOV) ACI protein (see AAW3336). It is encoded by a mutant ACI gene (see AAT93284) of tomato mottle virus virus (TOMOV), and carries 2 mutations in an NTP-binding domain. The ACI gene (see also AAT93294) must be expressed for efficient replication of the two genomic components, DNA-A and DNA-B, of the bipartite TOMOV genome. The invention involves production of transgenic plants containing DNA comprising geninivirus ACI or C1 wild-type or mutant sequences that negatively interfere in trans with geminiviral replication during infection. Such transgenic plants are resistant to viral infection. The ACI/C1 genes are especially from TOMOV, tomato yellow leaf curl virus or bean golden mosaic geminivirus (see AAT93282-93) and encode polypeptides (see AAW34324-35) that have mutations in the highly conserved DNA-nicking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mottle virus, tomato yellow leaf curl virus or bean golden mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and/or NTP-binding domains
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                                                                 PAIVLCNPGEGASYKEFLDKAENTGLKNWTVKNAIFITLTAPLYQDSTQASQETGNQKAQ
                                                                                   PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTQASQETGNQKAQ
                                                                                                                                                                   LSGHLDFNGRVFSNDVQYNVIDDIAPHYLKLKHWKELLGAQKDWQSNCKYGKPVQIKGGI
                                                                                                                                                                                                                           VPPFQVSSFTNVPDEMQEWADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMWARALGPHNY
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                                                                                                                                                                                                                                                                                                                                               LVQFEGKYQCTNNRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDTIEWGDFQIDG
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                                                                                                                                                                                                       VPPFQVSSFTNVPDEMQEWADNYFGTGAAARPERPVSIIVEGDSRTGKTMWARALGPHNY
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97.8%;
                                                                                                                                        /QYNVIKYIAPHYLKLKHWKELLG/
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Pred. No. 1.4e-167;
3; Mismatches 5;
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                  Matches 351; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 361 AA;
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                                          RSARGGQQSANDSYAKALNAGSVQSALAVLREEQPKDFVLQNHNIRSNLERIFAKAPEPW
                                                                                                                             LVQFEGKYQCTNNRFFHLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDTIEWGDFQIDG
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   RSARGGQQSANDSYAKALNASSVQSALAVLREEQPKDFVLQNHNIRSNLERIFAKAPEPW
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97.2%;
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Pred. No. 2.3e-166;
"" wismatches 7;
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VPPFQVSSFTNVPDEMQEWADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMWARALGPHNY 240

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RESULT 5
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA and hybrid DNA - used for recombinant vector of
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02-MAY-1991
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81; Conservative
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RSARGGQQSANDSYAKALNADSIESALTILKEEQPKDYVLQNHNIRSNLERIFFKVPEPW
                                                                                                     RSARGGQQSANDSYAKALNAGSVQSALAVLREEQPKDFVLQNHNIRSNLERIFAKAPEPW
                                                                                                                                                                          LIQFEGKFICTNKRLFDLVSTTRSAHFHPNIQGAKSSSDVKEYIDKDGVTIEWGQFQVDG
                                                                                                                                                                                                              LVQFEGKYQCTNNRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDTIEWGDFQIDG
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                                                                                                                                                                                                                                                                                                                                                                      Score 1575; DB 1;
Pred. No. 5.4e-138;
14; Mismatches 37;
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                       Query Match
Best Local S
                                                                                                                                                                                           This protein comprises a control mutant of the bean golden mosaic virus (BGMV) (1 protein (see AAW34338) that is required for replication. It is encoded by mutated C1 open reading frame BGAC190 (see AAT93290). The invention involves production of transgenic plants containing DNA comprising geminivirus C1 or AC1 wild-type or mutant sequences that negatively interfere in trans with geminiviral replication during infection. Such transgenic plants are resistant to viral infection. The AC1/C1 genes are especially from BGMV, tomato mottle virus or tomato yellow leaf curl virus (see AAT93282-93) and encode polypeptides (see AAW34324-35) that have mutations in the highly conserved DNA-nicking and/or the NTP-binding domains. (Updated on 17-OCT-2003 to standardise C
                                                                                                                                                                      and/or the field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato motile virus, tomato yellow leaf curl virus or bean golden mosaic
                                                                                                                 Sequence 353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stout JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Geminivirus; BGMV; C1 gene; transdominant mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bean golden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW34332;
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27-APR-1998
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                             Similarity
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Pred. No. 1e-137;
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                                                            This sequence comprises the bean golden mosaic virus (BGMV) C1 protein that is required for replication. The invention involves production of transgenic plants containing DNA comprising C1 or AC1 wild-type or mutant sequences that negatively interfere in trans with geminiviral replication during infection. Such transgenic plants are resistant to viral infection. The AC1/C1 genes are especially from BGMV, tomato mottle virus or tomato yellow leaf curl virus (see AAT93282-93) and encode polypoptides (see AAM9324-55) that have mutations in the highly conserved DNA-nicking domain and/or the NTP-binding domains. (Updated on 17-OCT-2003 to standardise OS field)
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27-APR-1998
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Sequence 353

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This protein comprises a transdominant lethal mutant of the bean golden mosaic virus (BGMV) Cl protein (see AAW34338) that is required for replication. It is encoded by mutated Cl pen reading frame BGAC221 (see AAT93291) and carries a mutation in the NTP-binding domain. The invention involves production of transgenic plants containing DNA comprising

Example 5; Page 107-109; 132pp; English.

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Matches
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Best Local Similarity
                                                                                                    genes - have i
                                                                                                    Transgenic plants expressing geminivirus AC1 and C1 wild-type and genes - have increased resistance to geminivirus infection e.g. to mottle virus, tomato yellow leaf curl virus or bean golden mosaic
                                                                                                                                                   WPI; 1997-526447/48.
N-PSDB; AAT93291.
                                                                                                                                                                                                                                                                                                                                                                                                Bean
                                                                                                                                                                                                                                                                   15-APR-1997;
                                                                                                                                                                                                                                                                                         23-OCT-1997
                                                                                                                                                                                                                                                                                                                 WO9739110-A1
                                                                                                                                                                                                                                                                                                                                      Bean golden mosaic virus; type II isolate Guatemala
                                                                                                                                                                                                                                                                                                                                                                         Geminivirus;
                                                                                                                                                                                                                                                                                                                                                                                                                      17-OCT-2003
27-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW34333;
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                                                                                                                                                                                                                                            16-APR-1996;
                                                                                                                                                                                                           (SEMI-) SEMINIS VEGETABLE SEEDS INC. (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                               golden
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                                                                                                                                                                                                                                                                                                                                                                                                mosaic geminivirus C1 BGA221 mutant.
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(first en
                                                                                                                                                                                                                                                                                                                                                                         BGMV;
                                                                                                                                                                                    HT,
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Pred No. 1e-137;
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                                                                                                                                                                                                                                                                                                                                                                          mutation;
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                                                                                                                                                                                                                                                                                                                                                                          transgenic plant;
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Best Local Sim
Matches 282;
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 Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato
                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                              17-OCT-2003
27-APR-1998
                                                          WPI;
                                                                                                                                                       16-APR-1996;
                                                                                                                                                                                  15-APR-1997;
                                                                                                                                                                                                            23-OCT-1997.
                                                                                                                                                                                                                                       WO9739110-A1
                                                                                                                                                                                                                                                               Bean golden mosaic virus;
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                                                                                                                                                                                                                                                                                                          Geminivirus;
                                                                                                                                                                                                                                                                                                                                 Bean golden mosaic geminivirus
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                                          1997-526447/48.
DB; AAT93292.
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                                                                                                             SEMINIS VEGETABLE SEEDS INC. WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                           resistance.
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(first en
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                                                                                  SF,
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Pred. No. 3e-137;
11; Mismatches 39;
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16-APR-1996;

15-APR-1997;

97WO-US006300 96US-0015517P

23-OCT-1997

WO9739110-A1

golden

mosaic

virus;

type

II isolate

Guatemala

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RESULT 10
AAW34335
ID AAW34
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XX 17-OC
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                              disease
                                                                                                                                                                                                                                                                                                                                           Geminivirus;
                                                                                                                                                                                                                                                                                                                                                                                               Bean golden
                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-OCT-2003
27-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW34335;
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                                                                                                                                                                                                                                                                                                              resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSIVLCNPGEGSSYKDFLDKEENRALHNWTIHNAIFVTLTAPLYQSTTQDCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPPFPLSSFINVPVVMQEWVDDYFGRGSAARPERPISIIVEGDSRTGHTMWARALGPHNY
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                                                                                                                                                                                                                                                                                                                                                                                            mosaic geminivirus C1 BGA262 mutant.
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                                                                                                                                                                                                                                                                                                                                        BGMV; C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
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80.1%; Pred. No. 3.76
tive 31; Mismatches
                                                                                                                                                                                                                                                                                                                                        gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; DB 2;
3.7e-137;
                                                                                                                                                                                                                                                                                                                                        mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bean golden mosaic
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                                                                                                                                                                                                                                                                                                                                        transgenic plant;
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RESULT 11
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Best Local Similarity
Matches 282; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This protein comprises a transdominant lethal mutant of the bean golden mosaic virus (BGMV) C1 protein (see AAM34318) that is required for replication. It is encoded by mutated C1 open reading frame BGAC262 (see AAT93292) and carries a mutation in the NTP-binding domain. The invention involves production of transgenic plants containing DNA comprising geminivirus C1 or AC1 wild-type or mutant sequences that negatively interfere in trans with geminiviral replication during infection. Such transgenic plants are resistant to viral infection. The AC1/C1 genes are especially from BGMV, tomato mottle virus or tomato yellow leaf curl virus (see AAT93282-93) and encode polypeptides (see AAM34324-35) that have mutations in the highly conserved DNA-nicking and/or the NTP-binding domains. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mother virus, tomato yellow leaf curl virus or bean golden mosaic
                                                                                                                                                 AAB18687;
                                                                                                                                                                                  AAB18687 standard;
Tomato golden mosaic virus.
                                 Geminivirus; replication ribosome binding region;
                                                                                 Amino acid sequence of a geminivirus replication protein of TGMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SEMI-) SEMINIS VEGETABLE SEEDS INC (WISC ) WISCONSIN ALUMNI RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Page 115-116;
                                                                                                                                                                                                                                                                                                                                                                                                                             VPPFQVSSFTNVPDEMQEWADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMWARALGPHNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVQFEGKYQCTNNRFFDLVSFTRSAHFHPNIQGAKSSSDVKSYIDKDGDTIEWGDFQIDG
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                                                                                                                                                                                                                                                                  LSGHLDFNGRVFSNDVQYNVIDDIAPHYLKLKHWKELLGAQKDWQSNCKYGKFVQIKGGI
                                                                                                                                                                                                                                                                                                                                                                                                     VPPFPLSSFINVPVVMQEWVDDYFGRGSAARPERPISIIVEGDSRTGKTMWARALGPHNY
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                                                                                                                                                                                                                                                                                                                                   LSGHLDFNSRVYSNAVEYNVIRDISPNYLKLKHWKELIGAQKDWQSNCKYGKPVQIKGGI
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                                                                                                                  (first
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80.1%;
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                                  resistance;
                                              protein; Rep protein; AL1; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31;
                                                                                                                                                                                    356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1564; DB 2;
Pred. No. 5.7e-137;
1; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maxwell
                                 geminivirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 353;
                                    infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a geminivirus replication (Rep) protein, which is also known as ALI. ALI binds double-stranded DNA, catalyses cleavage and ligation of single-stranded DNA, and interacts with other viral and host proteins. Mutants of the ALI protein are used to produce transgenic plants. The mutantion in ALI is present in a ribosome binding region, and expression of mutant ALI protein imparts increased resistance to geminivirus infection in the plant. Mutant ALI proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, comato yellow mosaic virus, ladian cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic plants with increased resistance to geminivirus infection comprise a nucleic acid construct containing a nucleic acid sequence encoding a mutant ALI protein with a mutation in the Rb binding regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 356 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 47-48; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-618851/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanley-Bowdoin L, Orozco BM,
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09-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                 301
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301
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                                                                                                                                                                                                                                                    121 RSARGGQQSANDSYAKALNAGSVQSALAVLREEQPKDFVLQNHNIRSNLERIFAKAPEPW
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                                                                                                                                                                                                                                                                                                             61 LVQFEGKYQCTNNRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDTIEWGDFQIDG
                                                                                                                                                                                                                                                                                                                                                                               MPSHPRFQINAKNYFLTYPQCSLSKEESLSQLQALNTPINKKFIKICRELHEDGQPHLHV
                        PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTQASQETGN 356
                                                                                          LSGHLDFNGRVFSNDVQYNVIDDIAPHYLKLKHWKELLGAQKDWQSNCKYGKPVQIKGGI
                                                                                                                                             LPPFHVSSFTNVPDEMRQWAENYFGKSSAARPERPISIIIEGDSRTGKTMWARSLGPHNY
                                                                                                                                                            | VPPFQVSSFTNVPDEMQEWADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMWARALGPHNY
                                                                                                                                                                                                               RSARGGCQTSNDAAAEALNASSKEEALQIIREKIPEKYLFQFHNLNSNLDRIFDKTPEPW
                                                                                                                                                                                                                                                                                        LIQFEGKYCCQNQRFFDLVSPTRSAHFHPNIQRAKSSSDVKTYIDKDGDTLVWGEFQVDG
PSIVLCNPGEGASYKVFLDKEENTPLKNWTFHNAKFVFLNSPLYQSSTQSSNNXNS
                                                                     LSGHLDLNSRVYSNKVEYNVIDDVTPQYLKLKHWKELIGAQRDWQTNCKYGKPVQIKGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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99US-00289346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "unspecified
                                                                                                                                                                                                                                                                                                                                                                                                                                 77.3%; Score 1499; DB 3; 74.4%; Pred. No. 6.8e-131; ative 45; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutation of consensus amino acids in the NTP-binding site of geminivirus Rep protein is used to produce replication deficient viruses. The mutated viral nucleic acid is used for producing transgenic plants that are resistant to, or tolerant of, the native virus. The present sequence is a mutant form of the Rep (or C1) protein from the Sardinian isolate of tomato yellow leaf curl virus (STYLCV) in which the wild-type Lys227 residue has been changed to an Arg residue; transgenic Nicotiana benthamiana plants generated by transformation with the mutated virus were not resistant to STYLCV. In contrast, plants transformed with a virus in which Lys227 had been replaced by Ala were found to be resistant. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modification; mutation; viral replication; deficient; inhibition; viral resistance; geminivirus; tomato yellow leaf curl virus; Sardinian isolate; STYLCV; transgenic plant; P-loop; Cl protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prodn. of virus-resistant transgenic plants -
sequence from phytopathogenic DNA virus.
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07-NOV-1996
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DB; AAT12906.
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VPPFQVSSFTNVPDEMQEW-ADNYFGTGDAAPPDRPVSIIVEGDSRTGKIMWARALGPHN
                                                                                                                    RSARGGQQSANDSYAKALNAGSVQSALAVLREEQPKDFVLQNHNIRSNLERIFAKAPEPW
                                                                                                                                                                         LIQFEGKYNCTNQRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDVLEWGTFQIDG
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                                                                           RSARGGQQTANDAYAKAINAGSKSQALDVIKELAPRDYVLHFHNINSNLDKVFQVPPAPY
                                                                                                                                                                                                                                                                      MPRSGRFSIKAKNYFLTYPKCDLTKENALSQITNLQTPTNKLFIKICRELHENGEPHLHI
                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                        Mutation of consensus amino acids in the NTP-binding site of geminivirus Rep protein is used to produce replication deficient viruses. The mutated viral nucleic acid is used for producing transgenic plants that are resistant to, or tolerant of, the native virus. The present sequence is a mutant form of the Rep (or Cl) protein from the Sardinian isolate of tomato yellow leaf curl virus (STYLCV) in which the wild-type Lys227 residue has been changed to a His residue; transgenic Nicotiana benthamiana plants generated by transformation with the mutated virus were not resistant to STYLCV. In contrast, plants transformed with a virus in which Lys227 had been replaced by Ala were found to be resistant. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide triphosphate binding site; DNA helicase; RNA helicase; modification; mutation; viral replication; deficient; inhibition; viral resistance; geminivirus; tomato yellow leaf curl virus; viral isolate; STYLCV; transgenic plant; P-loop; Cl protein;
     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prodn. of virus-resistant transgenic plants - sequence from phytopathogenic DNA virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-179947/18.
N-PSDB; AAT12905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sardinian tomato yellow leaf curl virus mutated Rep protein (K227H).
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07-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide triphosphate binding site; DNA helicase; RNA helicase; modification; mutation; viral replication; deficient; inhibition; viral restetance; genthivirus; tomato yellow leaf curl virus; sardinian isolate; STYLCV; transgenic plant; P-loop; C1 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sardinian tomato yellow leaf curl virus mutated Rep protein (K227A).
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                      Prodn. of virus-resistant transgenic plants - sequence from phytopathogenic DNA virus.
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227
/note= "wild-type L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "wild-type Lys has been replaced by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                virus.
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8; Mismatches 66; Indels
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Matches 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2003
27-APR-1998
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                          16-APR-1996;
                                                                                  15-APR-1997;
                                                                                                                                                                                              WO9739110-A1
                                                                                                                                                                                                                                                   Tomato yellow
                                                                                                                                                                                                                                                                                                           disease resistance
                                                                                                                                                                                                                                                                                                                                     Geminivirus; TYLCV; C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW34337;
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                                                                                                                                                                                                                                                                                                                                                                                          Tomato yellow leaf curl virus C1 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLY----QESTQASQETG
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                                                                                                                                                                                                                                                   curl virus; strain Israel
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                                                                                                                                                                                                                                                                                                                                  gene; transdominant mutation; transgenic plant;
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Best Local Similarity 66.3
Matches 238; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This protein comprises the wild-type C1 protein of tomato yellow leaf curl virus (TYLCV), a geminivirus that has a monopartite genome. The C1 protein is required for replication. The invention involves production of transgenic plants containing DNA comprising geminivirus AC1 or C1 wild-type or mutant sequences that negatively interfere in trans with geminiviral replication during infection. Such transgenic plants are resistant to viral infection. The AC1/C1 genes are especially from TYLCV, tomato mottle virus or bean golden mosaic geminivirus (see AAT93282-93) and encode polypeptides (see AAW34324-35) that can have mutations in the highly conserved DNA-nicking domain and/or the NTP-binding domain. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato motile virus, tomato yellow leaf curl virus or bean golden mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-526447/48.
N-PSDB; AAT93311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 357
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                                                                                                                                                                                                                                                                     124 RGGQQSANDSYAKALNAGSVQSALAVLREEQPKDFVLQNHNIRSNLERIFAKAPEPWVPP 183
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                                      IVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLY----QESTQASQETGNQ 357
                                                                                                    GHLDFNGRVFSNDVQYNVIDDIAPHYLKLKHWKELLGAQKDWQSNCKYGKPVQIKGGIPA 302
                                                                                                                                                                                     FQVSSFTNVPDEMQEW-ADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMWARALGPHNYLS 242
                                                                                                                                                                                                                                                                                                                              FEGKYQCTNNRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDTIEWGDFQIDGRSA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                PKKFRVQSKNYFLTYPQCSLSKBEALSQLQNLNTPVNKKFIKICRELHENGEPHLHVLVQ 63
                                                                                 GHLDLSPKVYSNDAWYNVIDDVNPHY--LKHFKEFIWAQRDWQSNTKYGKPIQIKGGIPT 297
                                                                                                                                                                FLSSSFNQVPDELEEWVAENV--VYSAARPWRPISIVIEGDSRTGKTMWARSLGPHNYLC 239
                                                                                                                                                                                                                                                 RGGQQSANDAYAEALNSGSISEALNILKEKAPKDYILQFHNLSSNLDRIFSPPLEVYVSP 181
                                                                                                                                                                                                                                                                                                                                                                                                              PRIFKIYAKNYFLTYPNCSLSKEEALSQLKKLETPTNKKYIKVCKELHENGEPHLHVLIQ 61
IFLCNPGPTSSYREYLDEEKNISLKNWALKNATFVTLYEPLFASINQGPTQDSQEETNK 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanson SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.7%; Score 1293.5; DB 2; 66.3%; Pred. No. 1e-111; tive 53; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maxwell DP,
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Result
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2 6/ptcdata/1/iaa/6A_COMB.pep:*
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Sequence 4, Appli
Sequence 44, Appli
Sequence 49, Appli
Sequence 52, Appli
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Sequence 7, Appli
Sequence 6, Appli
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RESULT 1  US-08-838-151A-2  US-08-838-151A-2  Sequence 2, Application US/08838151A  Patent No. 6291743  ; GENERAL INFORMATION:  APPLICANT: Lou, Hang T  APPLICANT: Lou, Hang T  APPLICANT: Maxwell, Douglas  APPLICANT: Ahlquist, Paul  APPLICANT: Hanson, Steve  TITLE OF INVENTION: Genes  TITLE OF INVENTION: Genes  NUMBER OF SEQUENCES: 63  ; CORRESPONDENCE ADDRESS:		w w	42 101.5 43 101.5		102.	37 102.5 38 102.5	102.	102.	102.	102.	102.	103.	103.	
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lants Expressing	ALIGNMENTS	US-09-543-681A-5122 US-09-248-796A-23610	US-08-811-949-55 5520913-1		5185259-3	US-08-883-795A-38 US-09-703-695A-4	US-08-560-098A-50	,	PCT-US91-01025A-2	US-09-612-314A-51	US-07-600-510B-16	US-09-600-985-3	US-09-600-985-2	
Geminivirus		nce nce	Sequence ! Patent No.	Patent No.	ö	Sequence Sequence					Seguence		Sequence	
			55, Appl 5520913	5344773	5185259	38, Appl 4, Appli	50, Appl		2, Appli	51, Appl	16 Appl	•		

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US-08-838-151A-2
  Matches 355;
                  Query Match
Best Local (
                                                                                                                                                                                                                                CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
                                                                                                                                                                                            TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/838,151A
                                                                                          LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Drestreet: Two Pacific Clify: Chicago
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                    Similarity
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Two Prudential Plaza, Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
    Conservative
98.4%; Score 1908; DB 3; 98.3%; Pred. No. 2.5e-189; tive 3; Mismatches 3;
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                                      Length 361;
    Indels
    0,
    Gaps
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US-08-838-151A-6; Sequence 6, Application US/08838151A; Patent No. 6291743
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                         TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
                                                                                                                                                         ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEPAX: 312-616-5460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgeni.
TITLE OF INVENTION: Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
                                                               TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
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: Illinois
                                                                                amino acid
XGY: linear
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                                                             protein
 98.1%;
98.1%;
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                                                                                                                                                                                                             SVS3801P0260
 Score 1902; DB 3;
Pred. No. 1e-188;
               Length
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                                           TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
                                                                                                                                                                                                                                                                                                                                                                   STREET: IT. Chicago CITY: Chicago Illinois
                                                                                                                           NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SYS
TELECOMMUNICATION INFORMATION:
 MOLECULE TYPE:
               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 60601
                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
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                                                                                                               312-616-5400
protein
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61 LVQFEGKYQCTNNRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDTIEWGDFQIDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MPPPKKFRVQSKNYFLTYPQCSLSKEEALSQLQNLNTPVNKKFIKICRELHENGEPHLHV
                      PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAFLYQESTQASQETGNQKAQ 360
                                                                                                                                  LSGHLDFNGRVFSNDVQYNVIDDIAPHYLKLKHWKELLGAQKDWQSNCKYGKPVQIKGGI
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                                                                                                      LSGHLDFNGRVFSNDVQYNVIDDIAPHYLKLKHWKELLGAQKDWQSNCKYGKPVQIKGGI
                                                                                                                                                                                                            VPPFQVSSFTNVPDEMQEWADNYFGTGAAARPERPVSIIVEGDSRTGHTMWARALGPHNY
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PAIVLCNPGEGASYKEFLDKAENTGLKNWTVKNAIFITLTAPLYQDSTQASQETGNQKAQ
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mielley Lies V GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Maxwell, Douglas
APPLICANT: Manyon, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCS ADDRESS: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700

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RESULT 4
US-08-838-151A-4
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Best Local
                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION UMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 312-616-5400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
               TELEFAX: 312-616-5460 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Trans.
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                 COUNTRY: U
                                                                                                                                                                                                                                                                                            CITY: Chicago
STATE: Illinois
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Luu, Hang T
Maxwell, Douglas
Ahlquist, Paul
Hanson, Steve
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97.8%;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44, Application US/08838151A Patent No. 6291743
GENERAL INFORMATION:
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Best Local Similarity
                          APPLICATION NUMBER: US/08/838
FILING DATE:
F
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APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transge
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Two Prud
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 60601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Dressler,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Dressler, Rockey, Milnamow & Katz
Two Prudential Plaza, Suite 4700
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Maxwell, Douglas
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                                     SVS3801P0260
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Pred. No. 4.7e-187;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acid
                         APPLICATION NUMBER: US/08/
FILING DATE:
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FILING DATE:
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ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
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Luu, Hang T
Maxwell, Douglas
Ahlquist, Paul
Hanson, Steve
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Matches 283; Company
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE SEATON acids
TENGTH: 353 amino acids
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TYPE: amino acid
TOPOLOGY: linear
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                                                 PSIVLCNPGEGSSYKDFLDKEENRALHNWTIHNAIFVTLTAPLYQSTTQDCQ 352
                                                                                 PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTQASQ 352
                                                                                                                           LSGHLDFNSRVYSNAVEYNVIDDISPNYLKLKHWKELIGAQKDWQSNCKYGKFVQIKGGI
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80.4%; Pred. No. 1.8e-154;
tive 31; Mismatches 38;
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US-08-838-151A-49 Sequence 49, Application US/08838151A Patent No. 6291743 GENERAL INFORMATION: APPLICANT: Stout, APPLICANT:
APPLICANT: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA: APPLICAN: Transcrittle OF INVENTION: Transcrittle OF INVENTION: Genes ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SV: ADDRESSEE: Dressler, APPLICANT: APPLICANT: FELECOMMUNICATION INFORMATION: FILING DATE: CLASSIFICATION: 800 CITY: Chicago STATE: Illinois APPLICATION NUMBER: COUNTRY: 60601 Stout, John T
Luu, Hang T
Maxwell, Douglas
Ahlquist, Paul
Hanson, Steve E: Dressler, Rockey, Milnamow & Katz Two Prudential Plaza, Suite 4700 U.S.A. Transgenic Plants Expressing Geminivirus US/08/838,151A SVS3801P0260 Version

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE: 63
                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: MUELLER, LIBS V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SV
                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
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                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                               CITY: Chicago
STATE: Illinois
                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                          COUNTRY:
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80.1%; Pred. No. 6e-154;
                                                                                                                    US/08/838,151A
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    SVS3801P0260
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:

ZIP: 60601

COUNTRY:

U.S.A.

Illinois

ATTORNEY/AGENT INFORMATION:
NAME: MUELler, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SV

SVS3801P0260

FILING DATE: APPLICATION NUMBER:

US/08/838,151A

#1.30

CLASSIFICATION:

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acid
                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transc
TITLE OF INVENTION: Genes
                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler,
                                                                                                                                                                                                       APPLICANT:
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                                                                                    NUMBER OF SEQUENCES:
CITY: Chicago
STATE: Illino
                                  STREET:
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                              E: Dressler, Rockey, Milnamow & Katz
Two Prudential Plaza, Suite 4700
                                                                                                                                                                     Luu, Hang T
Maxwell, Douglas
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                                                                                                                                                                                          , John T
Hang T
                                                                                                  Transgenic Plants Expressing Geminivirus Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.8%; Score 1566; DB 3;
80.1%; Pred. No. 7.6e-154;
ative 31; Mismatches 39;
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GENERAL INFORMATION:
APPLICANT: GRONENBORN, Bruno
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                          ZIP: 22202

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAtentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/08/809,103B
                                                                                CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
             APPLICATION NUMBER: WO POST FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 80.7%; Score 1564; DB 3; Local Similarity 80:1%; Pred. No. 1.2e-153; les 282; Conservative 31; Mismatches 39;
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                      CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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Y: U.S.A.
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                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08809103B Patent No. 6133505
GENERAL INFORMATION:
APPLICANT: GRONENBORN, Bruno
TITLE OF INVENTION: PHYTOPATHOGEN
TITLE OF INVENTION: TRANSGENIC PI
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Best Local Similarity 66.3%;
Matches 240; Conservative 4
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INFORMATION FOR SEQ ID NO:
                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
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TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEPHAX: (703) 685-0573
             CLASSIFICATION: 800 PRIOR APPLICATION DATA:
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LENGTH: 359 amino acid
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                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                               CITY: Arlington
STATE: Virginia
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APPLICATION NUMBER:
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Y: U.S.A.
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5 South 23rd Stree
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FR 94.11040
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Pred. No. 2.1e-127;
8; Mismatches 65;
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RESULT 12
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TELEFAX: (703) 685-0573
TELEFAX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
                                                                                                                                                                                                                                                                         Sequence 4, Application US/08809103B Patent No. 6133505
GENERAL INFORMATION:
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Best Local Similarity 66.0%;
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TYPE: amino acid
TOPOLOGY: lina
WOLECHT
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                             NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
                                                                                                                                                                                                                   APPLICANT: GRONENBORN, Bruno
TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
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REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 15-SEP-
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                                                                                       STREET: 745 South
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
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Pred. No. 4.2e-127;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: PATCH, Andrew J. REGISTRATION NUMBER: 32,925 REFERENCE/DOCKET NUMBER: US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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TELEFAX: (703) 685-0573
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                                                                       357 SE 358
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3.6e-127;
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Sequence 6, Application US/08809103B Patent No. 6133505

GENERAL INFORMATION:

APPLICANT: GRONENBORN, TITLE OF INVENTION: PH TITLE OF INVENTION: TR. NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:

ORN, Bruno PHYTOPATHOGENIC DNA VIRUS RESISTANT TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME

STREET: CITY: A

ADDRESSEE:

E: YOUNG & THOMPSON
745 South 23rd Street

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US-08-38-151A-20

US-08-38-151A-20

; Sequence 20, Application US/08838151A

; Patent No. 6291743

; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B FILING DATE: 17-MAR-1997 CLASSIFICATION: 800 PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040 FILING DATE: 15-SEP-1994 PRIOR APPLICATION NUMBER: WO PCT/FR95/01192 APPLICATION NUMBER: WO PCT/FR95/01192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 6:
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ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USBS
TELECOMMUNICATION INFORMATION:
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LENGTH: 359 amino acid
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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ZIP: 222
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703) 521-2297
TELEPAX: (703) 685-0573
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                                                                                                                                                                                                                                                                                                            YLCGHLDLSQKVYSNNAWYNVIDDVDPHY--LKHFKEFMGAQRDWQSNTKYGKPIQIKGG
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Stout, John T
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RESULT 15
US-08-838-151A-24
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Sequence 24, Application US/08838151A Patent No. 6291743 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REGISTRATION NUMBER: SVS3801P0260
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APPLICANT:
APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 312-616-5400
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SOFTWARE: PatentI
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CITY: Chicago
STATE: Illinois
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                                                                                                                                          IVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLY----QESTQASQETGNQ 357
                                                                                                                                                                                                                 GHLDFNGRVFSNDVQYNVIDDIAPHYLKLKHWKELLGAQKDWQSNCKYGKPVQIKGGIPA 302
                                                                                                                                                                                                                                                                                                                                   RGGQQSANDAYABALNSGSISBALNILKEKAPKDYILQFHNLSSNLDRIFSPPLEVYVSP
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                                                                                                                        IFLCNPGPTSSYREYLDEEKNISLKNWALKNATFVTLYEPLFASINQGPTQDSQEETNK 356
                                                                                                                                                                                            GHLDLSPKVYSNDAWYNVIDDVNPHY--LKHFKEFIWAQRDWQSNTKYGKPIQIKGGIPT
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Two Prudential Plaza, Suite 4700
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Maxwell, Douglas
Ahlquist, Paul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59;
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APPLICANT:

John

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELEPHONE: 312-616-5460
TELEPHONE: 312-616-5460
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APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                         303 IVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLY----QESTQASQETGNQ 357
                                                                                   240 GHLDLSPKVYSNDAWYNVIDDVDPHY--LKHFKEFMGAQRDWQSNTKYGKPIQIKGGIPT 297
                                                                                                                                                                           182 FLSSSFNQVPDELEEWVAENV--VYSAARPWRPISIVIEGDSRTGKTMWARSLGPHNYLC 239
                                                                                                                                                                                                                                                                                        124 RGGQQSANDSYAKALNAGSVQSALAVLREEQPKDFVLQNHNIRSNLERIFAKAPEPWVPP 183
298
                                                                                                                               243 GHLDFNGRVFSNDVQYNVIDDIAPHYLKLKHWKELLGAQKDWQSNCKYGKPVQIKGGIPA 302
                                                                                                                                                                                                       184 FQVSSFTNVPDEMQEW-ADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMWARALGPHNYLS 242
                                                                                                                                                                                                                                                                   122 RGGQQSANDAYAEALNSGSKSEALNILKEKAPKDYILQFHNLSSNLDRIFSPPLEVYVSP
                                                                                                                                                                                                                                                                                                                                                       4 PKKFRVQSKNYFLTYPQCSLSKEEALSQLQNLNTPVNKKFIKICRELHENGEPHLHVLVQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                               2 PRIFKIYAKNYFLTYPNCSLSKEEALSQLKKLETPTNKKYIKVCKELHENGEPHLHVLIQ 61
59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 357;
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Search completed: December 3, 2004, 15:02:11 Job time : 24 secs

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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
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                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution
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1939
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Listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published_Applications_AA:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/2/pubpaa/PCT_N
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m2_6/ptodata/2/pubpaa/ISO6_ENECOMB.pep:*
m2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
m2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
m2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
m2_6/ptodata/2/pubpaa/ISO8_NEW_PUB.pep:*
m2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
m2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
m2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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first 45 summaries
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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
ב	1908	98.4	361	اً ۵	US-08-838-151A-2	Sequence 2, Appli
N	1902	98.1	361	œ	US-08-838-151A-6	Sequence 6, Appli
ω	1892	97.6	361	œ	US-08-838-151A-8	
4	1886	97.3	361	œ	US-08-838-151A-4	Sequence 4, Appli
ហ	1572	81.1	353	œ	US-08-838-151A-44	44
a	1572	81.1	353	œ	US-08-838-151A-46	
7	1567	80.8	353	Ф	US-08-838-151A-49	
œ	1566	80.8	353	œ	US-08-838-151A-52	
9	1564	80.7	353	œ	US-08-838-151A-55	Sequence 55, Appl
_	1504.5	77.6	352	17	US-10-633-850-80	Sequence 80, Appl
11	1503.5	77.5	352	17	US-10-633-850-84	Sequence 84, Appl
12	1502.5	77.5	352	17	US-10-633-850-1	Sequence 1, Appli
13	1502.5	77.5	352	17	US-10-633-850-64	64,

## ALIGNMENTS

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US-08-838-151A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08838151A
Publication No. US20010011379A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Stout,
APPLICANT: Luu, Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Alquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                       CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mucller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SV
  TELECOMMUNICATION INFORMATION: TELEPHONE: 312-616-5400
                                                                                                                                                                                                                                                                                                                                                                            STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
TELEPHONE:
                                                                                                                                                        FILING DATE:
                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                     60601
                                                                                                                                                                                                                                                                                                                                                                                                                      E: Dressler, Rockey, Milnamow & Katz
Two Prudential Plaza, Suite 4700
                                                                                                                                                                                                                                                                                                                                                       U.S.A.
                                                                                                                                                                             US/08/838,151A
                                              SVS3801P0260
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS

2

TYPE: amino acids

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RESULT 2
US-08-838-151A-6
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                                                                                                                                                                                                                                                                                               Publication No. COLORD Publication No. COLORD Publication No. COLORD Publicant: Stout, John T APPLICANT: Etout, Hang T APPLICANT: Luu, Hang T APPLICANT: Maxwell, Douglas APPLICANT: Ahlquist, Paul APPLICANT: Hanson, Steve TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus; TITLE OF INVENTION: Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-838-151A-2
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Best Local Similarity 98.3
Matches 355; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08838151A Publication No. US20010011379A1
                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                              COUNTRY:
ZIP: 6060
                                               APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 800
                                                                                                                                                                                                                                                               STREET: Two Pr
                                                                                                                                                                                                                                                   STATE:
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                                                                                                                                                                       Floppy disk
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38,978
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Pred. No. 1.1e-162;
                                                                                                                         Version
                                                                                                                         #1.30
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08838151A Publication No. US20010011379A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 98.1%;
Best Local Similarity 98.1%;
Matches 354; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 312-616-5460 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transge
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                          APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/838,151A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: SV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS: LENGTH: 361 amino acid
                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                              COUNTRY: U.S.A. ZIP: 60601
                                                                                                                                                               CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
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Luu, Hang T
Maxwell, Douglas
Ahlquist, Paul
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Two Prudential
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al Plaza, Suite 4700
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Pred. No. 3.8e-162;
3; Mismatches 4;
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RESULT 4
US-08-838-151A-4
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                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08838151A Publication No. US20010011379A1 GENERAL INFORMATION:
APPLICANT: Stout, John T
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 8:
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ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SV63
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
                                                                                        STREET: LTC
CITY: Chicago
CITY: Illinois
                                                                                                                                                                              APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Mallat, Paul
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 361 amino acid
                                                                                                                                             ADDRESSEE: Dressler, Rockey, Milnamow & Katz STREET: Two Prudential Plaza, Suite 4700
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97.8%;
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TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-151A-4
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ATTORNAY AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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STREET: Two PrudicITY: Chicago STATE: Illinois COUNTRY: U.S.A. ZIP: 60601
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                                                                                            ADDRESSEE: Dressler,
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                                                                          E: Dressler, Rockey, Milnamow & Katz
Two Prudential Plaza, Suite 4700
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97.5%;
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Pred. No. 1e-160;
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                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                              Sequence 46, Application US/08838151A Publication No. US20010011379A1
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Best Local Similarity
                                                                                                               APPLICANT: Ahlquist, ....
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transge:
TITLE OF INVENTION: Genes
TITLE OF STOUENCES: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,9
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
                               CITY: Chicago
STATE: Illinois
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CLASSIFICATION:
                  COUNTRY:
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                U.S.A.
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Best Local Similarity
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                                                                              APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSE: Dressler, Rockey, Milnamow & Katz
                               CITY: Chicago
STATE: Illinois
                COUNTRY:
                                                                 STREET:
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                                                               E: Dressler, Rockey, Milnamow & Katz
Two Prudential Plaza, Suite 4700
                U.S.A.
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INFORMATION FOR SEQ ID NO: 46: SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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CLASSIFICATION: 800
CLASSIFICATION: 800
ATTORNEY_AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                  241 LSGHLDFNGRVFSNDVQYNVIDDIAPHYLKLKHWKELLGAQKDWQSNCKYGKPVQIKGGI
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                          PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTQASQ 352
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PSIVLCNPGEGSSYKDFLDKEENRALHNWTIHNAIFVTLTAPLYQSTTQDCQ
                                                                                                        LSGHLDFNSRVYSNAVEYNVIDDISPNYLKLKHWKELIGAQKDWQSNCKYGKPVQIKGGI
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80.4%; Pred. No. 1.7e-132;
ative 31; Mismatches 38;
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Best Local Similarity
Matches 282; Conserv
                                                                                                                                                                                                                                                                     Sequence 52, Application US/08838151A Publication No. US20010011379A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                      APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Maxwell, Deuglas
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                   CITY: Chicago
                                                                      STREET:
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                                                                    ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
                  COUNTRY:
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                              Illinois
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80.1%; Pred. No. 4.8e-132;
tive 31; Mismatches 39;
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                                                                                                                                                                                                                                                                                    Sequence 55, Application US/08838151A Publication No. US20010011379A1
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                      APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
                                                                                                        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                STREET: Two Pruc
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
                                                                                       ADDRESSEE: Dressler,
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E: Dressler, Rockey, Milnamow & Katz Two Prudential Plaza, Suite 4700

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US-08-838-151A-52
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,9
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
301
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XGY: linear
                  PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTQASQ 352
                                                                  RSARGGQQSANDSYAKALNADSIESALTILKEEQPKDYVLQHHNIRSNLERIFVKVPEPW
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PSIVLCNPGEGSSYKDFLDKEENRALHNWTIHNAIFVTLTAPLYQSTTQDCQ 352
                                                                                                                                            VPPFPLSFINVPVVMQEWVDDYFGRGSAARPERPISIIVEGDSRTGHTMWARALGPHNY
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Sequence 80, Application US/10633850
Publication No. US20040205843A1
GENERAL INFORMATION:
APPLICANT: Hanley-Bowdoin, Linda
APPLICANT: Orozco, Beverly M.
APPLICANT: Gruissem, Wilhelm
TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
FILE REFERENCE: 5051.4581P
CURRENT APPLICATION NUMBER: US/10/633,850
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 09/289,346
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin version 3.2
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Best Local Similarity
Matches 282; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acid
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TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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ID NO 80
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/838,151A FILING DATE:
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                                                                                                                                                                                                                                                                                                 US-10-633-850-84
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/125,004
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 84
SEQ ID NO 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 84, Application US/106 Publication No. US20040205843A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 267; Conserv
                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/633,850
CURRENT FILLING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 09/289,346
PRIOR FILLING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gruissem, Wilhelm
TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
FILE REFERENCE: 5051.4581P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hanley-Bowdoin, Linda APPLICANT: Orozco, Beverly M.
                                                                                                                                                                                                                                                                                                               LENGTH: 352
TYPE: PRT
ORGANISM: Tomato golden mosaic virus
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ORGANISM: Tomato
                                                                                                                                                                                                                                           Local Similarity
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121
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                                                                                          60 VLVQFEGKYQCTNNRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDTIEWGDFQID
                                                                    61 VLIQFEGKYCCQNQRFFDLVSPTRSAHFHPNIQRAKSSSDVKTVIDKDGDTLVWGEFQVD
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                                                                                                                                             1 MPSHPKRFQINAKNYFLTYPQCSLSKEBSLSQLQALNTPINKKFIKICRELHEDGQPHLH
                                                                                                                                                                          1 MPP-PKKFRVQSKNYFLTYPQCSLSKBBALSQLQNLNTPVNKKFIKICRELHENGEPHLH
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GRSARGGCQTSNDAAAEALNASSKEAALQIIREKIPEKYLFQFHNLNSNLDRIFDKTPEP
                               GRSARGGQQSANDSYAKALNAGSVQSALAVLREEQPKDFVLQNHNIRSNLERIFAKAPEP
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                                                                                                                                                                                                                     77.5%; Score 1503.5; DB 17; Length 75.9%; Pred. No. 2.4e-126; tive 45; Mismatches 39; Indels
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RESULT 13
US-10-633-850-64
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; ORGANISM: Tomato golden mosaic virus
US-10-633-850-1
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US-10-633-850-1
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CURRENT APPLICATION NUMBER: US/10/633,850
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 09/289,346
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 60/125,004
PRIOR APPLICATION NUMBER: US 60/125,004
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin version 3.2
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Sequence 64, Application US/10633850
Publication No. US20040205843A1
GENERAL INFORMATION:
APPLICANT: Hanley-Bowdoin, Linda
APPLICANT: Orozco, Beverly M.
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Publication No. US20040205843A1
GENERAL INFORMATION:
APPLICANT: Hanley-Bowdoin, Linda
APPLICANT: Orozco, Beverly M.
APPLICANT: Gruissem, Wilhelm
TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1
LENGTH: 352
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Best Local Similarity
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Publication No. US20040205843A1
GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 267; Conserv
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Best Local Similarity
                                                                                   TYPE: PRT ORGANISM: Tomato
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ORGANISM: Tomato
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   Conservative
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FILE REFERENCE: 5051.458IP
CURRENT APPLICATION NUMBER: US/10/633,850
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 09/289,346
PRIOR APPLICATION NUMBER: US 09/289,346
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 60/125,004
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 112
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TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 86
LENGTH: 352
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PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 60/125,004
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 112
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hanley-Bowdoin, Linda
APPLICANT: Orozco, Beverly M.
APPLICANT: Gruissem, Wilhelm
TITLE OF INVENTION: GEMINIVIRUS RESISTANT
FILE REFERENCE: 5051.4581P
CURRENT APPLICATION NUMBER: US/10/633,850
CURRENT FILING DATE: 2003-08-04
                                                                                                 golden mosaic virus
77.4%; Score 1500.5; DB 1 75.9%; Pred. No. 4.5e-126;
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44; Mismatches

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GENERAL INFORMATION:
APPLICANT: Halley-Bowdoin, Linda
APPLICANT: OTOZCO, Beverly M.
APPLICANT: GTUISSEM, WILHELM
TITLE OF INCENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
FILE REFERENCE: 5051.4581P
CURRENT APPLICATION NUMBER: US/10/633,850
CURRENT FILING DATE: 2003-08-04
PRIOR FILING DATE: 1099-04-09
PRIOR FILING DATE: 1099-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-03-18
VIMBER OF SEQ ID NUMBER: US 60/125,004
PRIOR FILING DATE: 1999-03-18
VIMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
CORGANISM: Tomato golden mosaic virus
US-10-633-850-82
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US-10-633-850-82
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                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 77.3
Best Local Similarity 75.9
Matches 267; Conservative
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                  YLSGHLDFNGRVFSNDVQYNVIDDIAPHYLKLKHWKELLGAQKDWQSNCKYGKPVQIKGG 299
                                                                                                                                                           GRSARGGCOTSNDAAAEALNASSKAEALQIIREKIPEKYLFQFHNLNSNLDRIFDKTPEP
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1939
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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                      MPPPKKFRVQSKNYFLTYPQ......PLYQESTQASQETGNQKAQG 361
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Copyright (c) 1993 - 2004 Compugen Ltd.
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QQCVS1
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AVI protein - bota
AVI protein - beet
ALI protein - toma
ALI protein - toma
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replicase - pepper
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replication-associ
replication-associ
ACI protein - Misca
CI protein - tobac
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RESULT 2
QCCVPT
ALL protein - potato yellow mosaic virus (isolate Venezuela)
ALL proteis: potato yellow mosaic virus
C;Species: potato yellow mosaic virus

Crossection process of the process o	30 31 31 32 32 33 34 34 35 37 37 38 39 40 40 41 41 41 41 41 41 41 41 41 41 41 41 41
C;Species: tomato mottle virus C;Species: tom. JQ1870 R;Abouzid, A.M.; Polston, J.E.; Hiebert, E. J. Gen. Virol. 73, 3225-3229, 1992 A;Title: The nucleotide sequence of tomato A;Reference number: JQ1869; MUID:93107858; A;Accession: JQ1870 A;Status: translation not shown A;Molecule type: DNA A;Residues: 1-358 <abo> A;Cross-references: UNIPROT:Q06657; GB:L144 C;Genetics: A;Map position: segment A C;Superfamily: tomato golden mosaic virus A C;Superfamily: lili                                  </abo>	191.5 188.5 187.5 161.5 102.5 102.5 98.5 98.5 96.9 96
Comacto mottle viator mottle viato mottle viator mottle viator mottle viator mottle viator mottle viator mottle sequen 19.87, 325-322.  73, 325-322.  73, 325-322.  73, 325-322.  701879.  70187	9.9 9.7 1148 9.7 1368 9.3 1368 9.3 1368 9.3 1368 5.4 979 5.0 2114 5.1 2114 5.1 2114 5.0 21
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PIDITION PED-1994 #text Peb-1994 #te	NTS
change 09-Jul-2004 a new geminivirus isolated icreLHENGEPHLHYLVQ 63	replication-associ hypothetical prote hypothetical 15.8K C1 protein - Panic replication-associ hypothetical prote t-plasminogen acti probable lipoprote myosin heavy chain hypothetical prote inorganic diphosph lytic murein trans hypothetical prote chitinase BH0916 [ nitric-oxide synth hypothetical prote chitinase BH0916 [ nitric-oxide synth hypothetical prote
<b>ä.</b>	

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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JU0364
R;Coutte, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
J. Gen. Virol. 72, 1515-1520, 1991
A;Title: The nuclectide sequence of the infectious cloned DNA components of potato yelld A;Reference number: JU0362; MUID:91311403; PMID:1856690
A;Accession: JU0364
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-361 <CCUb
A;Residues: 1-361 <CCUb
A;Cross-references: UNIPROT:P27258; GB:D00940; NID:g222458; PIDN:BAA00782.1; PID:g222459
C;Genetics:
A;Map position: segment A
C;Superfamily: tomato golden mosaic virus AL1 protein
     밁
                                                                                                                                                                                                                                                                                                                             AV1 protein - abutilon mosaic virus (isolate West India) C;Species: abutilon mosaic virus (;Spate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text. C;Accession: A36214 R;Frischmuth, T.; Zimmat, G.; Jeske, H. Virology 178, 461-468, 1990 A;Title: The nucleotide sequence of the abutilon mosaic A;Reference number: A36214; MUID:91020984; PMID:2219703 A;Accession: A36214
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C;Genetics:
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A; Residues: 1-355 < FRI>
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Best Local Similarity 77.9
Matches 279; Conservative
                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                 / Match 80.6%; Score 1562; DB 1; Local Similarity 81.4%; Pred. No. 3.8e-113; ses 293; Conservative 22; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 APPFPLSSTINVPDEMQEWADGYFGKSSAARPERPISIIIEGDSRRGKIMWARVLGPHNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 VPPFQVSSFTNVPDEMQEWADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMWARALGPHNY
     61
                      61 LVQFEGKYQCTNNRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDTIIEWGDFQIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LVQFEGKYQCTNNRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDTIEWGDFQIDG
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   LIQFEGKYQCTNNRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDTAEWGEFQIDG
                                                                            MPPPKKFRVQAKNYFLTYPQCSLTKDEALSQLQNLETPVNKKF1K1CRELHENGEPHLHV
                                                                                                 MPPPKKFRVQSKNYFLTYPQCSLSKEEALSQLQNLNTPVNKKFIKICRELHENGEPHLHV
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                                                                                                                                                                                                                        nt A
golden mosaic virus AL1 protein
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                                                                                                                                                                                                                                                                                 EMBL: X15983
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                                                                                                                                                   35;
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AL1 protein - beet curly top virus C;Species: beet curly top virus C;Date: 07-May-1993 #sequence_revision
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A;Modecule type: DNA
A;Residues: 1-352 <HAM's
A;Cross-references: UNIPROT:P03567
C;Comment: The genome consists of two circular, single-stranded DNA components, DNA A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: host Nicotiana sp. (tobacco)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change
C;Accession: A04170
R;Hamilton, W.D.O; Stein, V.E.; Coutts, R.H.A.; Buck, K.W.
EMBO J. 3, 2197-2205, 1984
A;Title: Complete nucleotide sequence of the infectious cloned I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: A04163
A;Accession: A04170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Superfamily:
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267; Conserv
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                                                                                                                                                                                                           WVPPFQVSSFTNVPDEMQEWADNYFGTGDAAPPDRFVSIIVEGDSRTGKTMWARALGPHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NYLSGHLDFNGRVFSNDVQYNVIDDIAPHYLKLKHWKELLGAQKDWQSNCKYGKPVQIKG
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                                                                                                               YLSGHLDFNGRVFSNDVQYNVIDDIAPHYLKLKHWKELLGAQKDWQSNCKYGKFVQIKGG
                                                                                                                                                                                                                                                                      GRSARGGCQTSNDAAABALNASSKEEALQIIREKIPEKYLFQFHNLNSNLDRIFDKTPEP
                                                                                                                                                                                                                                                                                                                 GRSARGGQQSANDSYAKALNAGSVQSALAVLREEQPKDFVLQNHNIRSNLERIFAKAPEP 179
                                                                                                                                                                                                                                                                                                                                                           VLIQFEGKYCCQNQRFFDLVSPTRSAHFHPNIQRAKSSSDVKTYIDKDGDTLVWGEFQVD
                                                                                                                                                                                                                                                                                                                                                                                                      VLVQFEGKYQCTNNRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDTIEWGDFQID
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                       IPAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTQAS
                                                                                     YLSGHLDLNSRVYSNKVEYNVIDDVTPQYLKLKHWKELIGAQRDWQTNCKYGKPVQIKGG
                                                                                                                                                                            WLPPFHVSSFTNVPDEMRQWAENYFGKSSAARPERPISIIIEGDSRTGKTMWARSLGPHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPSHPKRFQINAKNYFLTYPQCSLSKEESLSQLQALNTPINKKFIKICRELHEDGQPHLH
I PSI VLCNPGEGASYKVFLDKEENTPLKNWTFHNAKFVFLNSPLYQSSTQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tomato golden mosaic virus AL1 protein
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75.9%;
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; Pred. No. 1.5e-108;
44; Mismatches 40;
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07-May-1993 #text\_change 09-Jul-2004

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C;Date: 17-re. ... C;Accession: JQ1887 C;Accession: JQ1887 R;Dry, I.B.; Rigden, J.B.; Krake, R;Dry, Virol. 74, 147-151, 1993
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                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-362 < DRY>
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A; Accession: S28360
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R;Stanley, J; Markham, P.G.; Cal
EMBO J. 5, 1761-1767, 1986
A;Title: The nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                          L1 protein - tomato yellow leaf curl virus (strain ,Alternate names: C1 protein species: tomato yellow leaf curl virus (species: 17-Feb-1994 #sequence_revision 17-Feb-1994)
                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                            Cross-references: UNIPROT:P36279; GB:S53251
Superfamily: tomato golden mosaic virus AL1
                                                                                                                                                                                                                                                                                     Status: translation not shown
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Best Local Similarity
Matches 242; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Cross-references: UNIPROT:039485; GB:M24597; EMBL:X04144; NID:g210678; PIDN:AAA42751;Superfamily: tomato golden mosaic virus AL1 protein
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RSARGGQQSANDSYAKALNAGSVQSALAVLREEQPKDFVLQNHNIRSNLERIFAKAPEPW
                                                                                                                            MPPPKKFRVQSKNYFLTYPQCSLSKEEALSQLQNLNTPVNKKFIKICRELHENGEPHLHV
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                                                               LVQFEGKYQCTNNRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDTIEWGDFQIDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLQLEGKVQITNIRLFDLVSPTRSAHFHPNIQRAKSSSDVKSYVDKDGDTIEWGEFQIDG
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                                               LIQFEGKFQCKNQRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYLEKDGDTLEWGEFQIDG
                                                                                                         MTRPKSFRINAKNYFLTYPKCSLTKEEALSQLNNLETPTSKKYIKVCRELHENGEPHLHV
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69.8%;
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3; Mismatches 56
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ALI protein - pepper rizado amarillo virus C;Species: pepper rizado amarillo virus C;Date: 22-Nov-193 #sequence_revision 26-May C;Accession: S31875 R;Torres-Pacheco, I.; Garzon-Tiznado, J.A.; J submitted to the EMBL Data Library, Pebruary A;Description: Complete nucleotide sequence of A;Reference number: S31875 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      replicase - pepper huasteco virus (component A)
Nalternate names: ORF AL1 protein
C;Species: pepper huasteco virus
C;Species: pepper huasteco virus
C;Date: 14-Uul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: JQ2300
R;Torres-Pacheco, I:, Garzon-Tiznado, J.A.; Herrera-Estrella, L.; Rivera-Bus;
J. Gen. Virol. 74, 2225-2231, 1993
A;Title: Complete nucleotide of pepper huasteco virus: Analysis and comparis:
A;Reference number: JQ2299; MUJD:94015007; PMID:8409944
A;Recession: JQ2300
A;Recession: JQ2300
A;Residues: 1-349 <TOR>
A;Residues: 1-349 <TOR>
A;Coss-references: UNIPROT:Q06923; GB:X70418; NID:g61023; PIDN:CAA49856.1;
C;Superfamily: tomato golden mosaic virus AL1 protein
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Best Local S
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Pred. No. 7e-9
53; Mismatches
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sequence

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RESULT 9
$22593
hypothetical protein C4 - tomato yellow leaf curl virus
C;Species: tomato yellow leaf curl virus
C;Species: tomato yellow leaf curl virus
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: $22593
R;Kheyr-Pour, A.; Bendahmane, M.; Matzeit, V.; Accotto, G.P.; Crespi, S.; Gronenborn, B.
Nucleic Acids Res. 19, 6763-6769, 1991
A;Title: Tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monoparti
A;Reference number: $22588; MUID:92107660; PMID:1840676
A;Accession: $22593
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-359 <KHE>
A;Cross-references: UNIPROT:P27260; EMBL:X61153; NID:962211; PIDN:CAA43466:1; PID:962217
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
C;Superfamily: tomato golden mosaic virus Ail protein
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A; Residues: 1-349 <TOR>
A; Residues: UNIPROT:Q06923; EMBL:X70418; NID:g61023; PIDN:CAA49856.1;
A; Note: the source is designated as pepper huasteco virus
C; Superfamily: tomato golden mosaic virus ALI protein
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                        VSPFLSSSFDQVPDELEHWVSENVMDA--AARPWRPVSIVIEGDSRTGKTTWARSLGPHN
                                           VPPFQVSSFTNVPDEMQEW-ADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMWARALGPHN
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Pred. No. 7e-9
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Pred. No. 8.9e-94;
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AL1 protein - Indian cassava mosaic virus N;Alternate names: replication-associated C;Species: Indian cassava mosaic virus C;Date: 28-Aug-1985 #sequence_revision 07-C;Accession: JQ2327; S35883 R;Hong, Y.G.; Robinson, D.J.; Harrison, B.J. Gen. Virol. 74, 2437-2443, 1993
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A;Description: Nucleotide sequences from tomato leaf curl viru d geminiviruses.
A;Reference number: $58346
A;Accession: $59885
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-360 <HON>
A;Cross-references: UNIPROT:Q88557; EMBL:Z48182; NID:g944838; C;Superfamily: tomato golden mosaic virus AL1 protein
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R;Hong, Y.; Harrison, B.D.
submitted to the EMBL Data Library,
submitted to the EMBL Data Library,
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                                                                                          LCGHLDLSPRVYSNDAWYNVIDDVDPHY--LKHFKEFMGAQRDWQSNTKYGKPVQIKGGI
                                                                                                                                                                                       VSPFLCSSFDTVPEELHHWAAE--NVVDAAAAIRPISIVIEGDSRTGKTMWARSLGPHNY
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PTIFLCNPGPNSSYKEFLDEDKNNALKQWALKNATFITLEGPLYSGSNQSATQPSQE-GD
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ed protein 07-Oct-1994

#text\_change

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gene C1 protein - tomato yellow leaf curl virus
C;Species: tomato yellow leaf curl virus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09:Jul-2004
C;Accession: S39211
C;Accession: B39211
R;Noris, E.; Hidalgo, E.; Accotto, G.; Moriones, E.
submitted to the EMBL Data Library, August 1993
A;Description: High similarity among the tomato yellow leaf curl virus isolates from the A;Reference number: S39209
A;Accession: S39211
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-359 <NOR>
A;Cross-references: UNIPROT:P38609; EMBL:Z25751; NID:g433655; PIDN:CAA81026.1; PID:g4336C;Superfamily: tomato golden mosaic virus AL1 protein
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A;Accession: JQ2327
A;Molecule type: DNA
A;Residues: 1-351 <HON>
A;Cross-references: UNIPROT:Q82676; EMBL:Z24758; NID:g395351; PIDN:CAA80891.1; PID:g5840
C;Superfamily: tomato golden mosaic virus AL1 protein
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les 235; Conserv
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                          VPPFQVSSFTNVPDEMQEW-ADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMWARALGPHN
                                                                                                                                                                    LIQFEGKFNCKNNRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDVLEWGTFQIDG
                                                                                                                                                                                            LVQFEGKYQCTNNRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDTIEWGDFQIDG
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VSPFLSSSFDQVPDELEHWVSENVMDA--AARPWRPVSIVIEGDSRTGKTMWARSLGPHN
                                                                                 RSARGGOOTANDAYAKAINAGSKSEALDVIKELAPRDYILHFHNINSNLDRVFQVPPAPY
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ALI protein - tomato yellow leaf curl virus
N;Alternate names: C1 protein
C;Species: tomato yellow leaf curl virus
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
C;Accession: D40779
R;Navot, N.; Pichersky, E.; Zeidan, M.; Zamir, D.; Czosnek, H.
Virology 185, 151-161, 1991
A;Title: Tomato yellow leaf curl virus: a whitefly-transmitted graph a;Accession: D40779
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A; Residues: 1-357 <NAV>
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gene Cl protein - tomato yellow leaf curl virus C;Species: tomato yellow leaf curl virus C;Species: tomato yellow leaf curl virus C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change C;Accession: S39235 R;Crespi, S; Noris, E; Vaira, A; Bosco, D; Accotto, G. submitted to the EMBL Data Library, December 1993 A;Description: A cloned DNA from a TYLCV isolate from Sicily sho A;Reference number: S39233 A;Accession: S39233
A; Molecule type: DNA
A; Residues: 1-359 <CRE>
A; Cresterences: UNIPROT: Q88949; EMBL: Z28390; NID:g1041671;
C; Superfamily: tomato golden mosaic virus AL1 protein
                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S39235
                                                                                                                                                                                                                                                   showing
                                             PID:g1334964
                                                                                                                                                                                                                                                                                                                                                                                         09-Jul-2004
                                                                                                                                                                                                                                                      low infectivity
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hypothetical protein, 40.4K - cassava latent virus (Nigerian isolate)
(;Species: cassava latent virus
C;Date: 07-Sep-190  #sequence_revision 07-Sep-1990  #text_change 09-Jul-2004
C;Accession: $07594
R;Morris, B.; Coates, L.; Lowe, S.; Richardson, K.; Eddy, P.
Nucleic Acids Res. 18, 197-198, 1990
A;Title: Nucleotide sequence of the infectious cloned DNA components of African cassava
A;Reference number: $07590; MUID:90174930; PMID:2308831
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A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-358 <MOR>
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C;Superfamily: tomato golden mosaic virus AL1 protein
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C;Genetics:
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Best Local :
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                      186 VSSFTNVPDEMQEW-ADNYFGTGDAAPPDRPVSIIVEGDSRTGKTWWARALGPHNYLSGH 244
                                                                               125
                                                                                                           126 GQQSANDSYAKALNAGSVQSALAVLREEQPKDFVLQNHNIRSNLERIFAKAPEPWVPPFQ 185
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                                                                             GQQSANDAYAKALNSGSKSEALNVIRELVPKDFVLQFHNLNSNLDRIFQEPPAPYVSFFP
                                                                                                                                                        GKITITNNRLFDCVHPSCSTNFHPNIQGAKSSSDVKSYLDKDGDTVEWGQFQIDGRSARG
                                                                                                                                                                                 GKYQCTNNRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDTIEWGDFQIDGRSARG 125
                                                                                                                                                                                                                                     RFRVQAKNVFLTYPNCSIPKEHLLSFIQTLSLPSNPKFIKICRELHQNGEPHLHALIQFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YLSGHLDFNGRVFSNDVQYNVIDDIAPHYLKLKHWKELLGAQKDWQSNCKYGKPVQIKGG
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Search completed: December 3, 2004, 15:01:43
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   1640
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1: uniprot_sprot:*
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1939
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                               MPPPKKFRVQSKNYFLTYPQ......PLYQESTQASQETGNQKAQG 361
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                                                                                                                                                                                                                                                                                                                      Length DB
   VAL1 TMOV
Q67614
Q71963
Q11842
Q9YL74
Q7THT9
Q7THT9
Q36624
Q9J051
 Q9Q9R3
VAL1_BGMV
Q8QR22
                             Q8JMJ4
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Q9J049
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Q06657 tomato mott
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Q19163 sida golden
Q19174 chino del t
Q7tht9 tomato mott
Q36624 tomato mott
Q36624 tomato mott
Q36624 tomato mott
Q36624 tomato mott
Q36625 butilon mo
Q391049 chino del t
P89127 sida yellow
Q8jjv1 tobacco lea
Q67558 bean dwarf
Q71205 potato yell
P89122 sida golden
Q39nv9 sida golden
Q39nv9 sida golden
Q39nv5 sida golden
Q39nw5 sida golden
Q301w5 macroptiliu
Q3gn3 bean golden
Q30131 bean golden
Q30131 bean golden
Q80134 botato yell
Q41339 potato yell
Q41339 potato yell
Q41339 potato yell
Q5195 bean golden
Q718v7 sida golden
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P	8778	8888888888	R R R R R R R R R	\$222 <b>2</b> 222	V.R.	
Ouery Match  Best Local Similarity 100.0%; Score 1939,  Best Local Similarity 100.0%; Pred. No. 4,  Matches 361; Conservative 0; Mismatches  Oy 1	AL1_CLV AL1_CLV 1. ; 1. ; 1. ATP (B)	I SIMILARITY: Belongs to the site of the swiss institute of the European Bioinformatics Insective in the brooken this statement is officed and this statement is nitities requires a license agreement and the second and the statement is statement and the second and the secon	COUENCE FROM N.A.  SDLINE=93107858; PubMed=14693;  DOUZID A.M., Polston J.E., Hi  The nucleotide sequence of too  solated from tomatoes in Pior  Gen. Virol. 73:3225-3229(19)	AC Q06657; DT Q1-JUN-1994 (Rel. 29, Created) DT 01-JUN-1994 (Rel. 29, Last sequence update) DT 05-JUL-2004 (Rel. 44, Last annotation update DE AL1 protein. GN Name=AL1; OS Tomato mottle virus (isolate Florida) (TMOV) OC Viruses; ssDNA viruses; Geminiviridae; Begom OX NCBI TaxID=36449;	RESULT 1 VAL1_TMOV STANDARD; PRT; 361	32 1523 78.5 351 2 Q801H6 33 1522 78.5 358 2 Q70PB5 34 1522 78.5 358 2 CAD89709 35 1516 78.2 358 2 Q6R7R5 36 1516 78.2 358 2 Q6R7R5 37 1512 78.0 344 2 Q6R7Q8 38 1512 78.0 344 2 AAR95998 39 1512 78.0 344 2 AAR9597 39 15025 77.5 352 1 VAL1 TGMV 40 1498 77.3 361 2 Q67574 41 1497.5 77.2 349 2 Q8JNH1 42 1493 77.0 346 2 Q7TSV0 43 1489.5 76.8 352 2 Q9EQMG6 44 1483 76.5 352 2 Q9EQMG 45 1470 75.8 358 2 Q70PCO
SCORE 1939; DB 1; Length 361; Pred. No. 4.5e-143; Pred. No. 4.5e-143;  (CSLSKEEALSQLQNLNTPVNKKFIKICRELHENGEPHLHV 60)	similarity). SCEEAC6950 CRC64;	geminiviruses AL1 protein family.  Ight. It is produced through a collaboration bioinformatics and the EMBL outstation stitute. There are no restrictions on its stitute. There are no restrictions on its sons as long as its content is in no way not removed. Usage by and for commercial reement (See http://www.isb-sib.ch/announce/b-sib.ch).	us, a new gen	update) n update) ) (TMoV). s; Begomovirus.	MENTS	Q80ih6 dicliptera Q70pb5 sida micran Cad89709 sida micr Q6c775 tomato mosa Aar95968 tomato yell Aar95975 tomato yell Aar95975 tomato yell Aar95976 tomato golden Q6jhhi macroptiliu Q7t5v0 tomato chin Q8qmg6 tomato chin Q9pe000 tomato rugo Q70pc0 sida micran

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Q67614;
01-NOV-1996
01-NOV-1996
01-MAR-2004
                                                                                                                                                     GO; GO:0019028; C:viral capsid; IEA. GO; GO:005198; F:structural molecule InterPro; IPR001191; Gemini AL1. CLV. Pfam; PF00799; Gemini AL1; I.
                                                                                                                                                                                               Gilbertson R.L., Hiday: "Infectious DNA clones
                                                                                                                    PRINTS; PRO0227; GEMCOATALL.
PRINTS; PRO0228; GEMCOATCLVLI.
PRODOM; PRO000736; Gemini ALL; 1.
SEQUENCE 361 AA; 40547 MW; 3B3B2F75099A293C CRC64;
                                                                                                                                                                                                                                                         Gilbertson R.L., Hidayat
                                                                                                                                                                                                                                                                    MEDLINE=93139780;
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      Phytopathology 81:1184-1184(1991).
[2]
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NCBI_TaxID=10835;
                                                                                                                                                                                                                                                                                                                                                                  Tomato mottle virus.
                                                                                                                                                                                                                                                      Maxwell D.P.;
                                                                                                                                                                                                                                                                                                      in Florida.";
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                 19
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                 LVQFEGKYQCTNNRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDTIEWGDFQIDG
                               LVQFEGKYQCTNNRFFDLVSPTRSAHFHPNIQGAKSSSDVKSYIDKDGDTIEWGDFQIDG
                                                           MPPPKKFRVQSKNYFLTYPQCSLSKEEALSQLQNLNTPVNKKFIKICRELHENGEPHLHV
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RSARGGQQSANDSYAKALNAGSVQSALAVLREEQPKDFVLQNHNIRSNLERIFAKAPEPW 180
                                                   MPPPKKFRVQSKNYFLTYPQCSLSKEEALSQLQNLNTPVNKKF1K1CRELHENGEPHLHV
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clones of
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Hidayat S.H., Paplomatas E.J., Rojas M.R.,
                                                                                           98.4%;
98.3%;
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                                                                                 Score 1908; DD ., Pred. No. 1.2e-140;
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Last annotation update)
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w geminivirus associated
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                                                                                                                                                                                 activity;
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                                                                                                                                                                                  Matches
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Best Local
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01-AUG-1998
01-AUG-1998
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=51034;
                                                                                                                                                                                                                                                                                                                                                                Sida golden mosaic virus
Viruses; ssDNA viruses; (
                                                                                                                                                                                                                                                                                                                                                                                           Replication
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                                                                                                                                                                                       92.4%;
91.1%;
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A Abouzid A.M., Polston J.E., Hiebert E.;
A Abouzid A.M., Polston J.E., Hiebert E.;
L Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
C -!- SIMILARITY: Belongs to the geminiviruses AL1 protein f.
EMBL; AF049336; AAC05152.1; -.
R HSSP; P27360; LL51.
R GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
R GO; GO:0005198; F:structural AL1.
R InterPro; IPR001191; Gemini AL1.
R InterPro; IPR001301; Gemini AL1.
R InterPro; IPR001301; Gemini AL1.
R PRINTS; PR00227; GEMCOATCLVL1.
R PRINTS; PR00228; GEMCOATCLVL1.
R PRINTS; PR00228; GEMCOATCLVL1.
R PRINTS; PR00238; GEMCOATCLVL1.
R PRODOm; PD000736; Gemini AL1; 1.
R PrODOm; PD000736; Gemini AL1; 1.
R PRODOM; PD000736; Gemini AL1; 1.
                                                                                                                                                                                                                                                                                                                                                                                               1 MPPPKKFRVQSKNYFLTYPQCSLSKEEALSQLQNLNTPVNKKFIKICRELHENGEPHLHV
                                                                                             VPPFQVSSFTNVPDEMQEWADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMWARALGPHNY
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                                                                   VPPFQLSSFTNVPDEMQEWADEFFGSGSAARPDRPLSLIVEGDSRTGKIMWARALGPHNY
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(TrEMBLrel. 07, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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Pred. No. 1.4e-
20; Mismatches
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Best Local Similarity
Matches 319; Conserv
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-!- SIMILARITY: Balongs to the geminivir
EMBL; X15983; CAA34111.2; -.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:005198; F:structural molecule ac
Interpro; IPR001301; Gemini AL1.
Interpro; IPR001301; Gemini AL1.
PFAm; PF00799; Gemini AL1.
PRINTS; PR00227; GEMCOATAL1.
PRINTS; PR00228; GEMCOATCUL1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=ORF C1;
Abutilon mosaic virus.
Viruses; ssDNA viruses
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CHAIN 333 356 14.4 kDa
SEQUENCE 356 AA; 40247 MW; 3AA732:
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01-MAR-2004
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                                                                                                                                                                VPRFPLSSFTAVPEEMQEWADDYFGSGSAARPDRPLSLIVEGDSRTGKTMWARALGPHNY
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      PRELIMINARY;
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Last sequence that the control of the cont
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Pred. No. 2.1e
24; Mismatches
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      PRT;
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      361
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2.1e-129;
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AL1 protein
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Q7THT9
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AC Q7
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DT 01
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Best Local Similarity
Matches 316; Conserv
                                                                                                                           Q7THT9;
Q7THT9;
01-OCT-2003
01-OCT-2003
01-MAR-2004
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01-MAY-1999
01-MAY-1999
01-MAR-2004
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Guzman P., Gilbertson R.L.;

"Complete nucleotide sequence of the infectious c
crumple geminivirus.";

(In) Unknown A. (eds.);

ANNUAL MEETING OF THE AMERICAN PHYTOPATHOLOGICAL
ANNUAL MEETING OF THE AMERICAN PHYTOPATHOLOGICAL
PHYTOPATHOLOGY, VOL 88 (SUPPL), pp.44-0, Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001191; Gemini_AL1.
InterPro; IPR001301; Gemini_AL1_CLV.
Pfam, PP00799; Gemini_AL1; I.
PRINTS; PR00227; GEMCOATAL1.
PRINTS; PR00228; GEMCOATCLVI.
PRODOm; PD000736; Gemini_AL1; 1.
SEQUENCE 361 AA; 40826 MW; 7968527DD3A185B1
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Jiang H., Hou Y.-M., Guzman P., Gilbertson R.1

Jiang H., Hou Y.-M., Guzman P., Gilbertson R.1

Submitted (OCT-1998) to the EMBL/GenBank/DDBJ

-|- SIMILARITY: Belongs to the geminiviruses /

EMBL, AF101476; AAD17898.1; -.
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule
   Viruses; seDNA
                                     Tomato mottle Taino virus.
                                                                       Name=AC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC1 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSARGGOQSANDSYAKALNAGSVQSAMAVLKEEQPKDFVLHNHNIRSNLERIFAKAPERW
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                                                                                                                                                                                                                                                                   PRELIMINARY;
   viruses;
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88.3%; Pred. No. 3.3e-127;
Live 25; Mismatches 17;
      Geminiviridae;
                                                                                                                                 25,
26,
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Geminiviridae;
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Last annotation update)
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AL1 protein
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Matches
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"Taino tomato mottle virus, a new bipart plant Dis. 0:0-0(1997).

-- SIMILARITY: Belongs to the geminivi EMBL; AF012300; AAD09668.1; -.

HSSP; P27260; 1L51.
GO; GO:00019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule ac InterPro; IPR001191; Gemini_AL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cordero M., Ramos P.L., Hernandez L., Fernandez A.I., Eclevar A., Gonzalez G., Garcia D., Valdes S., Estevez A., Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AJ563919; CAD91703.1; -.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; F:structural molecule activity; IEA. InterPro, IPR001191; Gemini AL1.
Pfam; PF00799; Gemini AL1; I.
ProDom; PD00736; Gemini AL1; I.
                                                                                                                                                                                                                 036624;
01-JAN-1998
                                                                                                        SEQUENCE FROM N.A. Ramos P.L., Guerra O.,
                                                                                                                                                     Tomato mottle Taino virus.
Viruses; ssDNA viruses; Geminiviridae;
                                                                                                                                                                                 Replication
                                                                                                                                                                                          01-JAN-1998
01-MAR-2004
                                                                                                                                                                                                                                         036624
                                                                                               Rivera-Bustamante R.;
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nes 316; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 AA;
                                                                                                                                                                            (TTEMBLrel. 05, Created)
(TTEMBLrel. 05, Last sequence update)
(TTEMBLrel. 26, Last annotation update)
associated protein.
                                                                                                                                                                                                                                         PRELIMINARY;
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88.3%;
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40735 MW; 78E289146A769404 CRC64;
                                                                                                        Peral P.,
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             activity;
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Best Local
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Q9J051;
01-OCT-2000
01-OCT-2000
01-MAR-2004
               PRINTS;
                                                                                                                                                                                                                                                                   Brown J.K., Ostrow K.M., laris A.m., so
"Chino del tomate virus: relationships
identification of A component variants
                                                                                                                                                                                                                                                                                                                                                                                                                "Transmission, host range, and virus-vector relationships of chino tomate virus, a whitefly-transmitted geminivirus from Sinaloa, Mexico.";
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Pfam; PF00799; Gemini AL1; 1.
PRINTS; PR00227; GEMCOATCLVL1.
PRINTS; PR00228; GEMCOATCLVL1.
ProDom; PD000736; Gemini AL1; 1.
SEQUENCE 361 AA; 40722 MW; 3D43D231F8CC7FB5 CRC64;
                  Pfam; PF00799; Gemini AL1; 1.
PRINTS; PR00227; GEMCOATAL1.
PRINTS; PR00228; GEMCOATCLVL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chino del tomate virus-[H8]
Viruses; ssDNA viruses; Gem
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                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              Plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=AC1
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PD000736;
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(TrEMBLrel. 26, Last ann
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Pred. No. 4.1e-126;
4; Mismatches 20;
                                                                                                                                                                                                               geminiviruses
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ps to other begomoviruses
ts that affect symptom
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                                              Query Match
Best Local Similarity
Matches 313; Conserv
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Best Local
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Q96612;
O1-FEB-1997
O1-FEB-1997
                                                                                                                                                                                                                                                                                                                                                       Wu Z.C.Hu.J.S.Polston.J.E., Ullman D.E., Hiebert E.; Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: Belongs to the geminiviruses AL1 protein EMBL; U51137; AAB18173.1; --
HSSP; P27260; 1L51.
                                                                                                                                       PRINTS; PR00227; GEMCOATALL.

PRINTS; PR00228; GEMCOATCLVLL.

ProDom; PD000736; Gemini ALL;

SEQUENCE 361 AA; 40886 MW;
                                                                                                                                                                                                                                   GG; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule
InterPro; IPR001191; Gemini AL1.
InterPro; IPR001301; Gemini AL1.
Pfam; PF00799; Gemini AL1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wu Z.C., Hu J.S., Pollston J.E., Ullman D.E., Hiebert E.; "Complete nuclectide sequence of a non-vector transmissible strain abutllon mosaic geminivirus in Hawaii."; phyropathology 86:608-613(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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  MPPPKKFRVQSKNYFLTYPQCSLSKEEALSQLQNLNTPVNKKFIKICRELHENGEPHLHV
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                                            88.2%; Score 1711; DB 2; llarity 86.9%; Pred. No. 2.9e-125; Conservative 26; Mismatches 21;
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Pred. No. 1.4e-125;
                                                                                                                    1.
034D5A7608253CDC CRC64;
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Best Local S
Matches 310
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Q9J049;
01-OCT-2000 (TrEMBLrel. 15, C
01-OCT-2000 (TrEMBLrel. 15, I
01-MAR-2004 (TrEMBLrel. 26, I
Replication initiator protein
                                                                                                                                   PRINTS; PR00227; GEMCŌATAL1.
PRINTS; PR00228; GEMCOATCLVLI.
Probom; PD000736; Gemini ALI; 1.
SEQUENCE 361 AA; 40928 MW; 8
                                                                                                                                                                                    InterPro; IPR001191; Gemini_AL1.
InterPro; IPR001301; Gemini_AL1_CLV
Pfam; PF00799; Gemini_AL1; I.
                                                                                                                                                                                                                                              Phytopathology 90:546-552(2000).
- i- SIMILARITY: Belongs to the geminiviruses
EMBL, AF226665, AAF36708.1; -
HSSP; P27260; 1L51.
                                                                                                                                                                                                                                                                                                                                                                                           Brown J.K., Nelson M.R.;
"Transmission, host range, and virus-vector relationships of chino tomate virus, a whitefly-transmitted geminivirus from Sinaloa,
                                                                                                                                                                                                                       GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule
                                                                                                                                                                                                                                                                                              expression."
                                                                                                                                                                                                                                                                                                         Brown J.K., Ostrow K.M., Idris A.M., Stenger D.C.; "Chino del tomate virus: relationships to other begomovirusidentification of A component variants that affect symptom
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      Plant
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Viruses; ssDNA viruses; Geminiviridae;
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                                                                                                  Similarity
LVQFEGKYQCTNNRFFDLVSFTRSAHFHPNIQGAKSSSDVKSYIDKDGDTIEWGDFQIDG
                                     VPPFQVSSFTNVPDEMQEWADNYFGTGDAAPPDRPVSIIVEGDSRTGKTMWARALGPHNY
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                                                                                     Conservative
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86.6%; Pred. No. 3...
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P89127;
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PRINTS; PR00228; GEMCOATCLVL1.
ProDom; PD000736; Gemini AL1; 1.
SEQUENCE 361 AA; 40956 MW; D
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InterPro; IPR001301; Gemini_AL1_
Pfam; PF00799; Gemini_AL1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sida yellow vein virus.
Viruses; ssDNA viruses;
NCBI_TaxID=223321;
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GO; GO:0005198; F:structural molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC1 protein
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                                                                                                                               RSARGGQQTANDSYAKALNAGSVLGAMTVLKEEQPKDFVLQNHN
                                                                                                                                                                     RSARGGQQSANDSYAKALNAGSVQSALAVLREEQPKDFVLQNHNIRSNLERIFAKAPEPW
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VPPFQLSSFTNVPERMQEWADDYFGCDSAARPERPVSIIVEGDSRTGKTMWARALGPHNY
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85.8%; Pred. No. 1.3e-123;
85.8%; Pred. No. 1.3e-25;
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01-OCT-2002
01-OCT-2002
01-MAR-2004
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-!- SIMILARITY: Belongs to the geminiviruses ALI protein family. EMBL; AJ488768; CAD32806.1; -.
HSSP; P27260; 1L5I.
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PRINTS; PR00228; GEMCOATCLVLI.
PRODOR; PD000736; GEMINI ALL; 1.
SEQUENCE 361 AA; 41038 MW; 1291C2DC119EABA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0019028; C:viral capsid; IEA. GO; GO:005198; F:structural molecule InterPro; IPR001191; Gemini_AL1. InterPro; IPR001301; Gemini_AL1_CLV. Pfam; PF00799; Gemini_AL1; I.
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Tobacco leaf rugose virus.
Viruses; ssDNA viruses; Ge
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                                                        PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTQASQE-TGNQKA
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                                               PSIVLCNPGEGASYKDFLDKEENASLRNWTIKNAVFITLTAPLYQEGAQTIQEKEGNQET
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Matches 298
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A Ahlquist P.G., Russell D.R., Maxwell D.P.;
L Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
C -!- SIMILARITY: Belongs to the geminiviruses AL1 protein fan
EMBL; M88179; AAC32402.1; -.
R EMBL; M88179; AAC32402.1; -.
R HSSP; P27260; IL51.
R GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral capsid; IEA.
R GO; GO:005198; F:structural molecule activity; IEA.
R InterPro; IPR001191; Gemini AL1.
R InterPro; IPR001201; Gemini AL1.
R Pfam; PF00799; Gemini AL1; 1.
R Pfam; PF00799; Gemini AL1; 1.
R PFINTS; PR00227; GEMCOATCLUL1.
R PRINTS; PR00228; GEMCOATCLUL1.
R PRINTS; PR00228; GEMCOATCLUL1.
R PFINTS; PR00228; GEMCOATCLUL1.
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01-AUG-1998
01-AUG-1998
01-MAR-2004
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"Cloning of the complete DNA genomes of four bean-infecting geminiviruses and determining their infectivity by electric particle acceleration.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bean dwarf mosaic virus.
Viruses; ssDNA viruses; NCBI TaxID=10838;
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Best Local S
Matches 295
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EMBL; AF039031; AAC09254.1; -.

GO; GO:0019028; F:structural molecule activity; GO; GO:0005198; F:structural molecule activity; InterPro; IPR001191; Gemini ALL.

InterPro; IPR001301; Gemini ALL.

InterPro; IPR001301; Gemini ALL.

PFANNTS; PR00227; GEMCOATCLVL1.

PRINTS; PR00228; GEMCOATCLVL1.

PRODOM; PD000736; GEMINI ALL; I.

SEQUENCE 350 AA; 39567 MW; A08E3E3BFIA068FD
                                                                                                                                                                                                                                                                                                                                      P89122;
01-MAY-1997
01-JAN-1998
01-MAR-2004
  Central
J. Gen.
                      MEDLINE=98007646; PubMed=9349490; Frischmuth T., Engel M., Lauster S., Jeske H.; "Nucleotide sequence evidence for the occurrence of three distinct whitefly-transmitted, Sida-infecting bipartite geminiviruses in Central America.";
                                                                                                                                                                                                             Sida golden mosaic Honduras virus.
Viruses; ssDNA viruses; Geminiviridae;
NCBI_TaxID=223316;
                                                                                                                                               SEQUENCE FROM N.A. STRAIN=Honduras;
                                                                                                                                                                                                                                                                                                               AC1 protein.
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STRAIN-PYMV/TT;
TO TO THE STRAIN M.,
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Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
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84.5%;
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EMBL; Y11097; CAA71973.1; -.

HSSP; P27260; LL5I.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019028; C:viral capsid; IEA.

InterPro; IPR001191; Gemini_AL1.

InterPro; IPR001301; Gemini_AL1.

Pfam; PF00799; Gemini_AL1; I.

PRINTS; PR002207; GEMCGATAL1.

PRINTS; PR002207; GEMCGATCLUL1.

PRODOM; PD000736; Gemini_AL1; 1.

PSQUENCE 361 AA; 41137 MW; 5BE4C17CE1C7E4DF CRC64;
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